

Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IPAL Plate: 41 Row: g Column: 9  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 9994186  
 This clone has the following problem: frame shifted.

# FEATURES

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:4614150"  
 /tissue\_type="kidney"  
 /clone\_lib="NIH MGC\_75"  
 /lab\_host="DH10B"  
 /note="Vector: pDNR-LIB"

BASE COUNT 870 a 519 c 591 g 846 t

## ORIGIN

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 Best Local Similarity 99.7%; Pred. No. 3.6e-286;  
 Matches 1497; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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 QY 96 CACGCCCAAGTTTCTCATCTTATCCAGAAATACCGTCTTGGTATGGAGATTAGTA 155  
 DB 459 CACGCCCAAGTTTCTCATCTTATCCAGAAATACCGTCTTGGTATGGAGATTAGTA 518  
 QY 156 GCAGTAGAGGAAATGTATGATACAACTTACGTTTGTATGAAAGATTTCGGCTTGAAGAC 215  
 DB 519 GCAGTAGAGGAAATGTATGATACAACTTACGTTTGTATGAAAGATTTCGGCTTGAAGAC 578  
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 QY 336 CAAATTAGGATAGATTTGTATCTGATGAATATTTCTTCTGAAACAGGGTTCTGCATC 395  
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 DB 1719 GCTTAACCTAAAGTCCATGCTCGGCGCTAAATTCGTATTAATTAATCTGGA-TTTTTTTT 1778  
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 ACCESSION BC051876  
 VERSION BC051876.1 GI:30354290  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2655)

## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heiton, E., Kettman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257  
 12477932  
 2 (bases 1 to 2655)  
 Strausberg, R.  
 Direct Submission  
 Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue procurement: ATCC  
 cDNA Library preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www.shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAP Plate: 110 Row: P Column: 4  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186  
 This clone has the following problem: frame shifted.

## FEATURES

## source

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6527736"  
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BASE COUNT  
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Query Match 96.4%; Score 1481.4; DB 11; Length 2655;  
 Best Local Similarity 99.6%; Pred. No. 1.7e-285;  
 Matches 1495; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

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REFERENCE 1 (bases 1 to 969)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM10604 row: f column: 16  
High quality sequence stop: 764.  
Location/Qualifiers  
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Best Local Similarity 91.8%; Pred. No. 2.3e-145;  
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QY 981 TTGCCAGAGCTGTGCAGTGCAGTGGCTGATCTATTAGAGACGATGCGTTATCTCCA 1040  
DB 361 TTGCCAGAGCTGTGCAGTGCAGTGGCTGATCTATTAGAGACGATGCGTTATCTCCA 420  
QY 1041 TCCTTAATCTCAGTGTGTTTGCCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATCT 1100  
DB 421 TCCTTAATCTCAGTGTGTTTGCCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATCT 480  
QY 1101 GAAAGAGGAGATCAAAACAGAAATAGGAGTTGTGCAACAGCTCTTTTGGAGGAGGCGCT 1160  
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DEFINITION BG185961  
ACCESSION BG185961  
VERSION BG185961.1 GI:13707648  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 811)  
AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.  
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression  
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
MEDLINE 2127151  
PubMed 11329013  
COMMENT Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave., Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athersys.com  
High quality sequence stop: 485.  
Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 97.6%; Pred. No. 5.8e-143;		Matches 787; Conservative 1; Mismatches 17; Indels 1; Gaps 1;	
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QY	955	GATAGCCGCATCACACACAGCAGCTCTTCCAGAGCTGTGCAGTGCAGTGGCTGATTCCT	1014
Db	725	GATAGCCGCATCACACACAGCAGCTCTTCCAGAGCTGTGCAGTGGCTGATTCCT	784
QY	1015	ATTAGAGACGTATGCTTATCTCCA 1040	
Db	785	ATTAGAGACGTATGCTTATCTCCA 810	

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DEFINITION mRNA sequence.  
ACCESSION BG681390  
VERSION BG681390.1 GI:13912787  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1142)

NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: c9apbs-r@mail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10610 row: d column: 13 High quality sequence stop: 803. Location/Qualifiers 1..1142 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4752348" /tissue_type="squamous cell carcinoma" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NCI_CGAP_skn4" /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library." BASE COUNT 364 a 241 c 288 g 249 t ORIGIN		Query Match 49.4%; Score 758.8; DB 10; Length 1142; Best Local Similarity 96.2%; Pred. No. 3.1e-141; Matches 808; Conservative 1; Mismatches 28; Indels 3; Gaps 3;	
QY	417	CAATTTCACAGAGCTGTGAGTCTCTCAGTGTCTACCCCTTCAGCTTTGGCACTGGACCTG	476
Db	44	CAATTTCACAGAGCTGTGAGTCTCTCAGTGTCTACCCCTTCAGC-TTGGCACTGGACCTG	102
QY	477	CTTAATAATGCTATAAAGCTTTAGTACCTTTGGAAGACCTTATTGCATATCTTGAACCA	536
Db	103	CTTAATAATGCTATAAAGCTTTAGTACCTTTGGAAGACCTTATTGCATATCTTGAACCA	162
QY	537	GAGAGATGGCAGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAG	596
Db	163	GAGAGATGGCAGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAG	222
QY	597	GCCTTTGTTTTGGAGAAATCCAGAGTGGTGGATCTGAACTTCTTAACAGAGGAGTTA	656
Db	223	GCCTTTGTTTTGGAGAAATCCAGAGTGGTGGATCTGAACTTCTTAACAGAGGAGTTA	282
QY	657	AGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGA	716
Db	283	AGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGA	342
QY	717	ACCGATACCAATTTCTGGCCAGGTTGTCTCTGGTTTAAACCGTGTGGTGGGAACTGTGCC	776
Db	343	ACCGATACCAATTTCTGGCCAGGTTGTCTCTGGTTTAAACCGTGTGGTGGGAACTGTGCC	402
QY	777	TGTTGTCTCCAAATTTGCAATGCAATGTCTCAATGTGTCTCCCAAGCAAGTTTACTAAAAATAC	836
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QY	837	CACGAGTCTCTCAGTTGAGACCAASACCGGTGTCCAGGGGATTGCACAAATCACTCACCC	896
Db	463	CACGAGTCTCTCAGTTGAGACCAASACCGGTGTCCAGGGGATTGCACAAATCACTCACCC	522
QY	897	GACGTGGCCCTGGAGCAACCATGAGAGTGTGTGCTGTGTGTGTCAGAGGGAGCACAGGAGA	956
Db	523	GACGTGGCCCTGGAGCAACCATGAGAGTGTGTGCTGTGTGTGTCAGAGGGAGCACAGGAGA	582
QY	957	TAGCCGCATCACCAACAGCAGCTCTTCCAGAGCTGTGCAGTGGCTGATTCAT	1016
Db	583	TAGCCGCATCACCAACAGCAGCTCTTCCAGAGCTGTGCAGTGGCTGATTCAT	642

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QY 1017 TAGAGAACGTAATCGTTATCTCCATCTTAATCTCAGTTGTTGTTTCAAGGACCTTTCA 1076
DB 643 TAGAGAACGTAATCGTTATCTCCATCTTAATCTCAGTTG-TTGCTTCAAGGACCTTTCA 701

QY 1077 TCTTCAGGATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGC 1136
DB 702 TCTTCAGGATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGC 761

QY 1137 AACAGCTCTTTTGAAGAGGAGGCTTAAAGGACAGAGAAAGGCTTTC-AATCGTGAAG 1195
DB 762 AACAGCTCTTTGAAGAGGAGGCTTAAAGGACAGAGAAAGGCTTTC-AATCGTGAAG 821

QY 1196 AAAATTAAATGTTGTTAATTAATAGATACCAAGCTAGTTTTCAGAGTTTACCATGTACGTATT 1255
DB 822 AAAATTAAATGTTGTTAATTAATAGATACCAAGCTAGTTTTCAGAGTTTACCATGTACGTATT 881

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DEFINITION mRNA sequence.
ACCESSION BI870535
VERSION BI870535.1 GI:16044208
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 802)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M12030 row: i column: 02
High quality sequence stop: 791.
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 227 a 169 c 198 g 208 t
ORIGIN
Query Match 47.7%; Score 733; DB 12; Length 802;
Best Local Similarity 97.6%; Pred. No. 4.7e-136;
Matches 786; Conservative 1; Mismatches 11; Indels 7; Gaps 4;

QY 550 TGGACTTAGAAGATCTATATAGGCAACTTGGCACTTCTTGGCAAGGCTTTGTTTGG 609
DB 3 TGGACTTAGAAGATCTAT-TAGGCAACTTGGCACTTCTG---CAGGCTTTGTTTGG 57

QY 610 GAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTGAAGATTATACAGCT 669
DB 58 GAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTGAAGATTATACAGCT 117

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QY 670 GCACACCTCGTAACCTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCACTTT 729
DB 118 GCACACCTCGTAACCTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCACTTT 177

QY 730 TCTGGCCAGGTTGTCTCTCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTGTCTCCACA 789
DB 178 TCTGGCCAGGTTGTCTCTCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTGTCTCCACA 237

QY 790 ATTGCAATCAATCTCAATGTGTCCCAAGCAAGGTACTTAAATAATACCAGAGGTCTTTC 849
DB 238 ATTGCAATCAATGTGTGTCCCAAGCAAGGTACTTAAATAATACCAGAGGTCTTTC 297

QY 850 AGTTGAGACCAAAACCGGCTGTCCAGGGGATTGACAAATCACTCACCGAGTGGCCCTGG 909
DB 298 AGTTGAGACCAAAACCGGCTGTCCAGGGGATTGACAAATCACTCACCGAGTGGCCCTGG 357

QY 910 AGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAGCACAGGAGGATACCCGATCACCC 969
DB 358 AGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAGCACAGGAGGATACCCGATCACCC 417

QY 970 ACCAGCAGCTCTTGCCAGAGGCTGTGAGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGTATG 1029
DB 418 ACCAGCAGCTCTTGCCAGAGGCTGTGAGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGTATG 477

QY 1030 CGTTATCTCCATCTTAATCTCAGTGTGTGTTTGTCTCAAGGACCTTTCATCTTCAGGATTTA 1089
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QY 1090 CAGTGTATTTCTGAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTTTTG 1149
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QY 1209 GTATTAAATAGATCACCACTAGTTTTCAGAGTTTACCATTGACCTATTTCCACTAGCTGGGT 1268
DB 658 GTATTAAATAGATCACCACTAGTTTTCAGAGTTTACCATTGACCTATTTCCACTAGCTGGGT 717

QY 1269 TCTGTATTTTCAAGTCTTTTCGATACGCTTAAAGTAAATGTCAGTACAGGAAAAAACTGTG 1328
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RESULT 8
AK052947
LOCUS 2765 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
library, clone:D93001M08 product:platelet-derived growth factor,
C polypeptide, full insert sequence.
ACCESSION AK052947
VERSION AK052947.1 GI:26343118
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLES High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLES Normalization and subtraction of cap-trapper-selected cDNAs to

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prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20493374  
11042159

# JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuoka, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

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# JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S., and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

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# JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2765)

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# JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Adachi, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## TITLE

# JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
Location/Qualifiers

# FEATURES source

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QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGAGGAAATGTATGATGATCAAC 183  
Db 476 CAAGAAATATGGTCTGTTGGAGATTAGTTCAGTAGTAGTGAATGCGGATCCAGC 535  
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Db 536 TGACATTTCATGAGAGATTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATT 595  
QY 244 TTGTAGAAGTTGAGGAGCCAGTGTAGGAACTATATTAGGCGCTGGTGGTTCGTTA 303  
Db 596 TTGTAGAAGTTGAGGAGCCAGTGTAGGAAAGTGTATTTAGGACGCTGGTGGTTCGTTA 655  
QY 304 CTGTACAGGAAACAGATTCTTAAGGAAATCAAAATAGGATAAGATTGTATCTGATG 363  
Db 656 CTGTGCGAGAAAGAGAGCTTCTTAAGGAAATCATATCAGGATAAGATTGTATCTGATG 715  
QY 364 AATATTTTCCTTCTGAACAGAGGTTCTTGATCCATCAACATTTGTTCATGCCACAATTC 423  
Db 716 AGTATTTTCCATCTGAACCCGAGTTCTGTCATCCATACAGTATATCATGCCACAGTCA 775  
QY 424 CAGAGCTGTGAGTCTCTCAGTGTCTACCCCTTCAGCTTTCAGCTGGACCTGCTTAATA 483  
Db 776 CAGAAACCAACAGAGTCTCTCGGTTGTGCCCTTCATCTTTGTCAATGGACCTGCTCAACA 835  
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Qy 844 TCCCTCAGTGGACCAAAACCGTGTGCTGAGGAGTTCACAAATCACTCAGCAGCTGG 903  
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Qy 904 CCCTGGACCAATGAGGAGTGTGCTGCTGAGGAGGAGGACAGGAGGATAGCCGC 963  
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Db 1316 AGCCTTCGTAGCAGCAC 1332

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AK033734  
VERSION  
KEYWORDS  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Carninci, P. and Hayashizaki, Y.  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
Autors  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Izawa, M., Ohara, E., Kawai, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL  
MEDLINE  
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AUTHORS

Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

4  
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Bono, H., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavani, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Brownstein, M.J., Bult, C., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Washima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wyehaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 3244)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
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JOURNAL  
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REFERENCE  
AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
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JOURNAL  
MEDLINE  
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REFERENCE  
AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
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JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/  
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AK042767

Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, Clone:A730022g11 product:platelet-derived growth factor, C polypeptide, full insert sequence.

AK042767.1

GI:26335314

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Mateu, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,



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QY      964 ATCACCACGAGCAGCTC 980
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VERSION    CB309471.1 GI:28832181
KEYWORDS   EST.
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REFERENCE 1 (bases 1 to 769)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Dr. Eliot Spindel
           cDNA Library Preparation: CLONTECH
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: NCI-CGAP clone distribution information can be
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ACCESSION BC029099
VERSION    BC029099.1 GI:20809397
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REFERENCE 1 (bases 1 to 2893)
AUTHORS   Strausberg, R.
TITLE     Direct Submission
JOURNAL   Submitted (01-MAY-2002) National Institutes of Health, Mammalian
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           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           USA
           NIH-MGC Project URL: http://mgc.nci.nih.gov
           Contact: MGC help desk
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Gilbert Smith, Ph.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Baylor College of Medicine Human Genome
           Sequencing Center
           Center code: BCM-HGSC
           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
           Contact: amg@bcm.tmc.edu
           Gunaratne, P.H.; Garcia, A.M.; Lu, X.; Hulyk, S.W.; Hale, S.M.;
           Yoon, V.S.; Kowis, C.R.; Lawrence, S.; Martin, R.G.; Muzny, D.M.;
           Richards, S.; Gibbs, R.A.
           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
           Series: IRAC Plate: 35 Row: p Column: 20
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passed the following selection criteria: matched mRNA gi: 10242384  
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DB 799 CACTACAGTATTATCATGCCACAAGTCACAGAAACCCAGAGTCCTTGGTGTGCCCT 858
QY 456 TCAGCTTGGCCATGGACCTGCTTAAATGCTATAAATGCTTACCTTTAGTACCTTGGAGAC 515
DB 859 TCATCTTTGTCTATGGACCTGCTCAACAACTGTGACTGTGCTTCACTACCTTGGAGAG 918
QY 516 CTATTGCGATCTTGAACAGAGATGGCAGTGGACCTTAGAGATCTATATAGGCCA 575
DB 919 CTGATTCTGATCTAGAGCCAGATTCGATGGCAGTGACCTTGGACAGCTCTCAAGCCA 978
QY 576 ACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAATCCAGAGTGGTGGATCTG 635
DB 979 ACATGGCAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAGAAAGCAAGTGGTGAATCTG 1038
QY 636 AACCTTCTACAGAGGAGTGAATTTATACAGCTGCACTCTCTAATCTCTCAGTGTCC 695
DB 1039 AATCTCTAAAGGAAGAGTAAATCTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCC 1098
QY 696 ATAGGGAAGAACTAAAGAGAACCGATACCACTTTCTGGCCAGGTTGCTCTCTGTTAAA 755
DB 1099 ATACGGGAAGAGCTAAAGAGAGACAGATACCATATTTCTGGCCAGGTTGCTCTCTGTCAG 1158
QY 756 CGCTGTGTGGGAAGTGTGCTGTGTGCTCCACAAATTCGAATGAATGCAATGTGTGCCA 815
DB 1159 CGCTGTGGGAAGATTTGGCTGTGTGCTCCATTAATTCGAATGAATGTCAGTGTGTCCCA 1218
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QY 816 AGCAAGCTTACTAAAAATACACGAGGTCTTTCAGTTGAGACCAAAACCGGTGTCTAGG 875
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QY 876 GGATTGCACAAATCACTACCGAGTGGCCCTGAGCACCACCATGAGGATGTGACTGTGTG 935
DB 1279 GGATTGCATAAGTCACTCATTTGATGTGGCTCTGGAACACCAACGAGGAATGTGACTGTGTG 1338
QY 936 TGCAAGGGAGCAGCAGGAGGATAGCCCATCACACACGACGACGCTC 980
DB 1339 TGTAGAGAAACGCGAGGAGGTAACCTGAGGCTTCGTAGGACGAC 1383
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RESULT 13
LOCUS      B0015321/c
DEFINITION UI-H-ED1-axw-j-04-0-UI.sl NCI CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5834595 3', mRNA sequence.
ACCESSION  B0015321
VERSION     B0015321.1 GI:19740222
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 686)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-re@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
POLYA-Yes
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      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:5834595"
      /tissue_type="Chondrosarcoma"
      /dev_stage="Adult"
      /lab_host="DH10B (Life Technologies)"
      /clone_lib="NCI CGAP ED1"
      /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
      (Pharmacia) with a modified polylinker; Site 1: EcoR I;
      Site 2: Not I; NCI CGAP_ED1 is a normalized cDNA library
      containing the following tissue(s): Chondrosarcoma cell
      line C85. The library was constructed according to Bonaldo
      , Lennon and Soares, Genome Research, 6:791-806, 1996.
      First strand cDNA synthesis was primed with an oligo-dT
      primer containing a Not I site. Double stranded cDNA was
      ligated to an EcoR I adaptor, digested with Not I, and
      cloned directionally into pT7T3-Pac vector. The
      oligonucleotide used to prime the synthesis of
      first-strand cDNA contains a library tag sequence that is
      located between the Not I site and the (dT)18 tail. The
      sequence tag for this library is GCTCAAGGCT.
      TAG_LIB=UI-H-ED1
      TAG_ISSUE=chondrosarcoma
      TAG_SEQ=CGTCAAGGCT"
BASE COUNT      197 a 152 c 130 g 207 t
ORIGIN
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Query Match 41.7%; Score 640; DB 12; Length 686;  
Best Local Similarity 98.7%; Pred. No. 1.7e-117;

Matches	665; Conservative	1; Mismatches	6; Indels	2; Gaps	2;
Qy	859	CAAAACCGGTGTGACGGGATTGCAAAATCACTCACCGAGTGGCCCTGGAGCACCATG			918
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Qy	919	AGGAGTGTGACTGTGTGTCAGAGGGAGCAGAGGATAGCCGATCACCCACGACGAC			978
Db	627	AGGAGTGTGACTGTGTGTCAGAGGGAGCAGAGGATAGCCGATCACCCACGACGAC			568
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Qy	1099	CTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGGAGGAGGC			1158
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Qy	1339	CCTGATTCGGTTCGCTTGTAACTCTAAAGCTCCATGCTCGGGCTTAAATCGTATAA			1398
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Db	27	GCTGATAGGAAAA 14			
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AK081347					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
PUBMED					
REFERENCE					
AUTHORS					

TITLE	
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to
MEDLINE	prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	20499374
AUTHORS	11042159
3	
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,	
Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M.,	
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20530913	
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,	
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Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P.,	
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and Hayashizaki, Y.	
Functional annotation of a full-length mouse cDNA collection	
Nature 409 (6821), 685-690 (2001)	
21085660	
11217851	
5	
The FANTOM Consortium and the RIKEN Genome Exploration Research	
Group Phase I & II Team.	
Analysis of the mouse transcriptome based on functional annotation	
of 60,770 full-length cDNAs	
Nature 420, 563-573 (2002)	
6 (bases 1 to 2502)	
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Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N.,	
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Segabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,	
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,	
Muramatsu, M. and Hayashizaki, Y.	
Direct Submission	
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of	
Physical and Chemical Research (RIKEN), Laboratory for Genome	
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),	
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,	
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,	
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,	
Fax: 81-45-503-9216)	
cDNA library was prepared and sequenced in Mouse Genome	
Encyclopedia Project of Genome Exploration Research Group in Riken	
Genomic Sciences Center and Genome Science Laboratory in RIKEN.	
Division of Experimental Animal Research in Riken contributed to	





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Db 321 GCCTAGAGGAAATGATGATACAACTTACGTTTGTGTAAGAGATTGGGCTTGAAGAC 380
Qy 216 CCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCCAGTGTGAACT 275
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Qy 456 TCAGCTTTGCCACTGGACCTGCTTAATAATGCTATACTGCTTTAGTACCTTTGGAAGAC 515
Db 621 TCAGCTTTGCCACTGGACCTGCTTAATAATGCTATACTGCTTTAGTACCTTTGGAAGAC 680
Qy 516 CTTATTCGATATCTTGAACCAAGAGATGGCAGTTGGACTTAGAAGATCTATAGGCCA 575
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Search completed: November 26, 2003, 05:47:49  
Job time : 2245.94 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:13 ; Search time 33.125 Seconds  
(without alignments)  
1523.775 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GKFQSSNKQNGVQFQHE.....DVALEHHEBCDCVCRGSTGG 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1728	99.7	345	20	AA1984558
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7	1728	99.7	345	21	AA1984558
8	1728	99.7	345	21	AA1984558
9	1728	99.7	345	21	AA1984558

10	1728	99.7	345	21	AA1984558
11	1728	99.7	345	21	AA1984558
12	1728	99.7	345	21	AA1984558
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#### ALIGNMENTS

#### RESULT 1

AA1984558

ID AA1984558 standard; Protein; 318 AA.

XX AC

XX AC

XX AC

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DE 25-JUL-2000 (first entry)

XX A fragment of platelet-derived growth factor C (PDGF-C).

XX Platelet-derived growth factor C; PDGF-C; cell proliferation;

XX growth factor; heparin; connective tissue; wound healing; VEGF-F;

XX fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;

XX choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;

XX lung carcinoma; erythroleukemia; tissue remodelling.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX Key

XX Misc-difference 287

XX /note= "encoded by AAS"

XX XX

XX WO200018212-A2.

XX PD

XX 06-APR-2000.

XX XX

XX 30-SEP-1999; 99WO-US22668.

XX XX

XX 30-SEP-1998; 98US-0102461.

XX 12-NOV-1998; 98US-0108109.

XX 03-DEC-1998; 98US-0110749.

XX 18-DEC-1998; 98US-0113002.

XX XX

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PR 21-MAY-1999; 99US-0135426.
PR 15-JUL-1999; 99US-0144022.
XX (LUDM-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX Erikson U, Aase K, Lee X, Ponten A, Dutela M, Alitalo K;
PI Oestman A, Heidin C, Betscholz C;
XX WPI: 2000-292954/25.
DR N-PSDB; AAA12524.
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor -
XX Disclosure; Fig 4; 135pp; English.
XX The present sequence represents a human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
CC the ability to stimulate and enhance proliferation or differentiation,
CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
CC especially found in the lung, kidney or liver.
XX Sequence 318 AA;
SQ Query Match 100.0%; Score 1734; DB 21; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.6e-167;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GKQFSSNKQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTLVWRLVAEENVWIIQ 60
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Db 61 LTDERFGLDPEDDICKYDFVEEESDGTILGRWCGSGTVPGKQISKGNQIRFVSD 120
QY 121 EYFSPGFCIHYNVMPQTEAVSPVLPPSLPLDLLNNAITAFSTLEDLIRYLEPER 180
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QY 301 ALEHHEECDCVCRGSTGG 318
Db 301 ALEHHEECDCVCRGSTGG 318
RESULT 2
AAY33679
ID AAY33679 standard; Protein; 345 AA.
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AY33679;

11-JAN-2000 (first entry)

Human VEGF-E protein.

VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.

Homo sapiens.

WO9947677-A2.

23-SEP-1999.

10-MAR-1999; 99WO-US05190.

17-MAR-1998; 98US-0040220.

02-NOV-1998; 98US-0184216.

(GETH ) GENENTECH INC.

Ferrara N, Kuo SS;

WPI; 1999-580306/49.

N-PSDB; AAZ23691.

New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy -

Claim 1; Fig 2; 122pp; English.

This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquilizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy. It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.

SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 20; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KFOFSSNKQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTLVWRLVAEENVWIIQ 61

Db 29 KFOFSSNKQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTLVWRLVAEENVWIIQ 88

```
QY      62  TFDERFGLPEDDICKYDFVEVEBPDSGTTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db      89  TFDERFGLPEDDICKYDFVEVEBPDSGTTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
QY     122  YFSEPGFCIHYNIVMQFTFAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
Db     149  YFSEPGFCIHYNIVMQFTFAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLEPERW 208
QY     182  QLDLEDLYRPTWQLLKAFVFGKRKSRVVDLMLLTFEEVRLYSCTPRNFVSISREELKRTDT 241
Db     209  QLDLEDLYRPTWQLLKAFVFGKRKSRVVDLMLLTFEEVRLYSCTPRNFVSISREELKRTDT 268
QY     242  IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
Db     269  IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 328
QY     302  LEHHECDCVCRGSTGG 318
Db     329  LEHHECDCVCRGSTGG 345

RESULT 3
AAY41766
ID  AAY41766 standard; Protein; 345 AA.
XX
AC  AAY41766;
XX
XX  07-DEC-1999 (first entry)
XX
XX  Human PRO200 protein sequence.
XX
KW  Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW  probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW  secreted protein; transmembrane protein.
XX
XX  Homo sapiens.
XX
XX  WO9946281-A2.
XX
PD  16-SEP-1999.
XX
PF  08-MAR-1999; 99WO-US05028.
XX
PR  10-MAR-1998; 98US-0077450.
PR  11-MAR-1998; 98US-0077632.
PR  11-MAR-1998; 98US-0077641.
PR  11-MAR-1998; 98US-0077649.
PR  12-MAR-1998; 98US-0077791.
PR  13-MAR-1998; 98US-0078004.
PR  17-MAR-1998; 98US-0040220.
PR  20-MAR-1998; 98US-0078886.
PR  20-MAR-1998; 98US-0078910.
PR  20-MAR-1998; 98US-0078936.
PR  20-MAR-1998; 98US-0078939.
PR  25-MAR-1998; 98US-0079294.
PR  26-MAR-1998; 98US-0079456.
PR  27-MAR-1998; 98US-0079663.
PR  27-MAR-1998; 98US-0079664.
PR  27-MAR-1998; 98US-0079689.
PR  27-MAR-1998; 98US-0079728.
PR  30-MAR-1998; 98US-0079786.
PR  30-MAR-1998; 98US-0079920.
PR  31-MAR-1998; 98US-0079923.
PR  31-MAR-1998; 98US-0080105.
PR  31-MAR-1998; 98US-0080107.
PR  31-MAR-1998; 98US-0080165.
PR  31-MAR-1998; 98US-0080194.
PR  01-APR-1998; 98US-0080327.
PR  01-APR-1998; 98US-0080328.
PR  01-APR-1998; 98US-0080333.
PR  01-APR-1998; 98US-0080334.
PR  08-APR-1998; 98US-0081049.
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PR  08-APR-1998; 98US-0081070.
PR  08-APR-1998; 98US-0081071.
PR  09-APR-1998; 98US-0081195.
PR  09-APR-1998; 98US-0081203.
PR  09-APR-1998; 98US-0081229.
PR  15-APR-1998; 98US-0081817.
PR  15-APR-1998; 98US-0081838.
PR  15-APR-1998; 98US-0081952.
PR  15-APR-1998; 98US-0081955.
PR  21-APR-1998; 98US-0082568.
PR  21-APR-1998; 98US-0082569.
PR  22-APR-1998; 98US-0082700.
PR  22-APR-1998; 98US-0082704.
PR  23-APR-1998; 98US-0082804.
PR  23-APR-1998; 98US-0082767.
PR  23-APR-1998; 98US-0082796.
PR  27-APR-1998; 98US-0083336.
PR  28-APR-1998; 98US-0083322.
PR  29-APR-1998; 98US-0083392.
PR  29-APR-1998; 98US-0083495.
PR  29-APR-1998; 98US-0083496.
PR  29-APR-1998; 98US-0083499.
PR  29-APR-1998; 98US-0083500.
PR  29-APR-1998; 98US-0083545.
PR  29-APR-1998; 98US-0083554.
PR  29-APR-1998; 98US-0083558.
PR  30-APR-1998; 98US-0083559.
PR  05-MAY-1998; 98US-0083742.
PR  06-MAY-1998; 98US-0084366.
PR  06-MAY-1998; 98US-0084414.
PR  06-MAY-1998; 98US-0084441.
PR  07-MAY-1998; 98US-0084598.
PR  07-MAY-1998; 98US-0084600.
PR  07-MAY-1998; 98US-0084627.
PR  07-MAY-1998; 98US-0084637.
PR  07-MAY-1998; 98US-0084639.
PR  07-MAY-1998; 98US-0084640.
PR  13-MAY-1998; 98US-0084643.
PR  13-MAY-1998; 98US-0085323.
PR  13-MAY-1998; 98US-0085338.
PR  15-MAY-1998; 98US-0085339.
PR  15-MAY-1998; 98US-0085573.
PR  15-MAY-1998; 98US-0085579.
PR  15-MAY-1998; 98US-0085580.
PR  15-MAY-1998; 98US-0085582.
PR  15-MAY-1998; 98US-0085689.
PR  15-MAY-1998; 98US-0085697.
PR  15-MAY-1998; 98US-0085700.
PR  18-MAY-1998; 98US-0085704.
PR  22-MAY-1998; 98US-0086023.
PR  22-MAY-1998; 98US-0086392.
PR  22-MAY-1998; 98US-0086414.
PR  22-MAY-1998; 98US-0086430.
PR  28-MAY-1998; 98US-0086486.
PR  28-MAY-1998; 98US-0087098.
PR  28-MAY-1998; 98US-0087106.
PR  30-JUL-1998; 98US-0087208.
PR  11-SEP-1998; 98US-0094651.
PR  98US-0100038.
```

(GETH ) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

N-PSDB; AAZ34296.

New secreted and transmembrane polypeptides and their polynucleotides,  
useful for treating blood coagulation disorders, cancers and cellular  
adhesion disorders -

Claim 12; Fig 207; 530pp; English.

XX



XX 03-MAY-2000; 2000WO-US40047.  
XX 03-MAY-1999; 99US-0304216.  
PR 10-NOV-1999; 99US-0164463.  
PR 04-FEB-2000; 2000US-0180169.  
XX (ZYMO) ZYMOGENETICS INC.  
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
XX WPI; 2000-687541/67.  
DR N-PSDB; AAC81582.  
XX Growth factor homologs and the nucleic acids that encode them, useful  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease -  
XX Claim 48; Page 125-126; 143pp; English.  
PS The invention relates to the human growth factor homologue zvegfg4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)  
CC characterised by a PDGF cysteine knot structure, and a CUB domain  
CC (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like  
CC activity, having mitogenic activity on fibroblasts, vascular smooth  
CC muscle cells and pericytes, and has also been shown to stimulate bone  
CC growth. The invention also relates to fusion proteins comprising human  
CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3  
CC fusions; expression constructs and host cells comprising human zvegfg4  
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody  
CC which binds to human zvegfg4 or a fragment thereof; a method of activating  
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a  
CC method of modulating the proliferation, differentiation, migration or  
CC metabolism of bone cells, comprising exposing bone cells to  
CC zvegfg4-derived polypeptides; and a method of detecting a genetic  
CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived  
CC fragments may be used to stimulate tissue development or repair, or  
CC cellular differentiation or proliferation. They are particularly used for  
CC the treatment or repair of liver damage, and may also be used to  
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
CC multiple sclerosis). Due to their osteogenic activity, they may be used  
CC in the treatment of periodontal disease and fractures. They may also be  
CC used to enhance expansion and mobilisation of haematopoietic stem cells  
CC and endothelial precursor stem cells, which may be useful in the  
CC treatment of ischaemia, in wound healing, and in the modulation of the  
CC immune system. The present sequence represents human zvegfg3.  
XX  
SQ Sequence 345 AA;  
Query Match 99.7%; Score 1728; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQGVDPQHERITVTSTNGSIHSPRPHTYPRNTVLVWELVAEENVMQL 61  
DB 29 KQFSSNKEQGVDPQHERITVTSTNGSIHSPRPHTYPRNTVLVWELVAEENVMQL 88  
QY 62 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 121  
DB 89 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 148  
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLIRPFWOLLGKAFVGRKSRVVDNLNLTVEVRLYSCPTPNFVSIREELKRTDT 241  
DB 209 QLDLEDLIRPFWOLLGKAFVGRKSRVVDNLNLTVEVRLYSCPTPNFVSIREELKRTDT 268  
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKHYEVLQLRPKTVGRGLHKLSTDA 301

DB 269 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKHYEVLQLRPKTVGRGLHKLSTDA 328  
QY 302 LEHHEECDCVCRGSGTGG 318  
DB 329 LEHHEECDCVCRGSGTGG 345  
RESULT 6  
AAB24250  
XX ID AAB24250 standard; Protein; 345 AA.  
XX AC AAB24250;  
XX DT 08-FEB-2001 (first entry)  
XX DE Human platelet-derived growth factor related protein LP8.  
XX KW Human; platelet derived growth factor related protein; LP8; VEGFh;  
KW vascular endothelial growth factor h; tissue regeneration; vulnerary;  
KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.  
XX OS Homo sapiens.  
XX PN WO200059940-A2.  
XX PD 12-OCT-2000.  
XX PF 24-MAR-2000; 2000WO-US06427.  
XX PR 06-APR-1999; 99US-0127913.  
XX (ELTL) LILLY & CO ELI.  
XX PI Hammond LJ, Na S;  
XX WPI; 2000-664991/64.  
DR N-PSDB; AAC64426.  
XX Enhancing tissue growth and promoting wound healing by administering  
PT platelet-derived growth factor related protein, LP8 or its analog and  
PT treating atherosclerosis by administering LP8 antagonist -  
XX Claim 4; Page 63-64; 64pp; English.  
XX The present invention describes a method for enhancing tissue growth,  
CC promoting wound healing or stimulating smooth muscle growth by  
CC administering a platelet-derived growth factor (PDGF) related protein,  
CC designated LP8 or its analogue. Also described is a method of slowing  
CC the progress of atherosclerosis or treating atherosclerosis comprising  
CC the administration of an LP8 antagonist. The method is useful for  
CC enhancing tissue growth, promoting wound healing and stimulating smooth  
CC muscle growth. Antagonists of LP8 are useful for treating  
CC atherosclerosis. The present sequence represents human LP8, which is  
CC also called VEGFh.  
XX  
SQ Sequence 345 AA;  
Query Match 99.7%; Score 1728; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQGVDPQHERITVTSTNGSIHSPRPHTYPRNTVLVWELVAEENVMQL 61  
DB 29 KQFSSNKEQGVDPQHERITVTSTNGSIHSPRPHTYPRNTVLVWELVAEENVMQL 88  
QY 62 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 121  
DB 89 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 148  
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208



182 QLDLEDLYRPTWLLGKAFVGRKSRVVDLNLITTEEVRLXSCPTPRNFVSIRBELKRTDT 241  
 209 QLDLEDLYRPTWLLGKAFVGRKSRVVDLNLITTEEVRLXSCPTPRNFVSIRBELKRTDT 268  
 242 IFWPGCLLVRCGGNACCLHNCNECQVPSKTKYHEVLQRLPKTVGRGLHSLTDVA 301  
 269 IFWPGCLLVRCGGNACCLHNCNECQVPSKTKYHEVLQRLPKTVGRGLHSLTDVA 328  
 302 LEHHECDVCVCRGSGTG 318  
 329 LEHHECDVCVCRGSGTG 345

RESULT 7  
 AAB44322  
 ID AAB44322 standard; Protein; 345 AA.  
 AC AAB44322;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.  
 XX  
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053756-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-US04341.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 29-MAR-1999; 99US-0126773.  
 PR 21-APR-1999; 99US-0130232.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 16-DEC-1999; 99WO-US28565.  
 PR 30-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 05-JAN-2000; 99WO-US31274.  
 PR 08-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Rilyvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,  
 PI Goddard A, Godowski P, Grimaldi CU, Gurney AL, Hillan KJ;  
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX  
 XX WPI; 2000-611443/58.  
 DR N-PSDB; AAC78582.  
 XX

Novel PRO polypeptides and polynucleotides used in detection methods,  
 to target bioactive molecules to specific cells, and to modulate  
 cellular activities .

Claim 12; Fig 207; 636pp; English.

AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 sequence tag) sequences which encode secreted or transmembrane PRO  
 polypeptides. The PRO polynucleotides and polypeptides have cytostatic

CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWIQL 61  
 DB 29 KQFSSNKEQGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWIQL 88  
 QY 62 TFDERFGLDEPDIDCKYDFVEVEEPESDGTILGRWCGSGTVPGKQISKGNQIRFVSDE 121  
 DB 89 TFDERFGLDEPDIDCKYDFVEVEEPESDGTILGRWCGSGTVPGKQISKGNQIRFVSDE 148  
 QY 122 YFSEPGFCHYNTVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERW 181  
 DB 149 YFSEPGFCHYNTVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERW 208  
 QY 182 QLDLEDLYRPTWLLGKAFVGRKSRVVDLNLITTEEVRLXSCPTPRNFVSIRBELKRTDT 241  
 DB 209 QLDLEDLYRPTWLLGKAFVGRKSRVVDLNLITTEEVRLXSCPTPRNFVSIRBELKRTDT 268  
 QY 242 IFWPGCLLVRCGGNACCLHNCNECQVPSKTKYHEVLQRLPKTVGRGLHSLTDVA 301  
 DB 269 IFWPGCLLVRCGGNACCLHNCNECQVPSKTKYHEVLQRLPKTVGRGLHSLTDVA 328  
 QY 302 LEHHECDVCVCRGSGTG 318  
 DB 329 LEHHECDVCVCRGSGTG 345

## RESULT 8

AAB10633  
 ID AAB10633 standard; Protein; 345 AA.

AC AAB10633;

DT 19-JAN-2001 (first entry)

DE Human RACE generated VEGF-X protein.

KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
 KW antiinflammatory; antiarthritic; antipsoriatic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

PN WO200037641-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99WO-US30503.

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC ) JANSSEN PHARM NV.

XX Gordon RD, Sprengel J, Yon JR, Dijkmans JH, Gosiewska A;  
 PI Dhanaraj SN, Xu J;



Db 329 LEHHECDCVCRGSGTG 345

RESULT 10

AA10644

ID AAB10644 standard; Protein; 345 AA.

XX

AC AAB10644;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human VEGF-X protein #4.

XX

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.

XX

OS Homo sapiens.

XX

PN W0200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

XX (JANSEN PHARM NV.

XX

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

DR N-PSDB; AAA71990.

XX

XX New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX

PS Disclosure; Fig 30B; 127pp; English.

XX

XX This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein described in the method of the invention.

XX

SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVDPQHERITVTSGSIHSPFPHYPTNTVLVRLVAVERNWIQL 61

Db 29 KQFSSNKEQGVDPQHERITVTSGSIHSPFPHYPTNTVLVRLVAVERNWIQL 88

62 TFDERFGLDEPDDICKYDFEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121

89 TFDERFGLDEPDDICKYDFEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148

122 YFPSEPGFCIHYNIVMPQFTTEAVSPSVLPSPALPLDLNNNAITAFSTLEDLIRVLEPERW 181

149 YFPSEPGFCIHYNIVMPQFTTEAVSPSVLPSPALPLDLNNNAITAFSTLEDLIRVLEPERW 208

182 QLDLEDLYRPTWOLLGKAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241

209 QLDLEDLYRPTWOLLGKAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268

242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKYHEVLQLRPKTGVRGLHSLTDVA 301

269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKYHEVLQLRPKTGVRGLHSLTDVA 328

302 LEHHECDCVCRGSGTG 318

329 LEHHECDCVCRGSGTG 345

RESULT 11

AA10650

ID AAB10650 standard; Protein; 345 AA.

XX

AC AAB10650;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human 990126veg protein.

XX

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.

XX

OS Homo sapiens.

XX

PN W0200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

XX (JANSEN PHARM NV.

XX

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

DR N-PSDB; AAA71990.

XX

XX New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX

PS Disclosure; Fig 11; 127pp; English.

XX

XX This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein described in the method of the invention.

XX

SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVDPQHERITVTSGSIHSPFPHYPTNTVLVRLVAVERNWIQL 61

Db 29 KQFSSNKEQGVDPQHERITVTSGSIHSPFPHYPTNTVLVRLVAVERNWIQL 88

CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human 990126vegX protein  
 CC used to illustrate the method of the invention.

XX  
 SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 61  
 Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 88  
 Qy 62 TFDERFGLDEDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121  
 Db 89 TFDERFGLDEDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148  
 Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNATFSTLEDLIRYLEPERW 181  
 Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNATFSTLEDLIRYLEPERW 208  
 Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 241  
 Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 268  
 Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYEVLQRLPKTVGRGLHKS LTDVA 301  
 Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYEVLQRLPKTVGRGLHKS LTDVA 328  
 Qy 302 LEHHECDCVCRGSGTG 318  
 Db 329 LEHHECDCVCRGSGTG 345

## RESULT 12

AA10651  
 ID AAB10651 standard; Protein; 345 AA.

AC AAB10651;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #3.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
 KW antiarthritis; antipsoaritic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US030503.

XX 22-DEC-1998; 98GB-00283377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC ) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;

XX Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -  
 XX Claim 72; Fig 12; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has  
 CC vulnery, cytostatic, antirheumatic, antiarthritis, antipsoaritic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human VEGF-X protein  
 CC described in the method of the invention.

XX Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 61

Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 88

Qy 62 TFDERFGLDEDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121

Db 89 TFDERFGLDEDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148

Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNATFSTLEDLIRYLEPERW 181

Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNATFSTLEDLIRYLEPERW 208

Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 241

Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 268

Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYEVLQRLPKTVGRGLHKS LTDVA 301

Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYEVLQRLPKTVGRGLHKS LTDVA 328

Qy 302 LEHHECDCVCRGSGTG 318

Db 329 LEHHECDCVCRGSGTG 345

## RESULT 13

AA19578

ID AAB19578 standard; Protein; 345 AA.

XX AAB19578;

XX 22-JAN-2001 (first entry)

XX Human PRO200 (vascular endothelial growth factor B).

XX PRO200; vascular epithelial growth factor B; VEGF-B; human;  
 KW ocular disease; retinopathy; maculopathy; therapy;  
 KW retinitis pigmentosa; macular degeneration; retinal detachment;  
 KW retinal tear; macular hole; myopia; traumatic chorioretinopathy;  
 KW acute retinal necrosis syndrome; contusion; edema;  
 KW retinal vision occlusion; vascular disease; retinal vasculitis;  
 KW thrombocytopenic purpura; uveitis; retinal occlusion.

OS Homo sapiens.

XX Key Location/Qualifiers

FH 1..14

FT /label= Signal\_peptide

FT Protein 15..345

FT /label= Mature\_Pro200 25..29

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site 55..59 /note= "Asn is N-glycosylated"

FT Modified-site 254..258 /note= "Asn is N-glycosylated"

FT Modified-site 15..21 /note= "N-myristoylation"

FT Modified-site 117..123 /note= "N-myristoylation"

FT Modified-site 127..133 /note= "N-myristoylation"

FT Modified-site 281..287 /note= "N-myristoylation"

FT Modified-site 282..288 /note= "N-myristoylation"

FT Modified-site 319..325 /note= "Amidation"

FT WO200053760-A2.

XX PD 14-SEP-2000.

XX PF 10-MAR-2000; 2000WO-US06319.

XX PR 12-MAR-1999; 99US-0123957.

XX PA (GETH ) GENENTECH INC.

XX PI Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;

XX PI Klein RD, Kljavin IU, Kuo SS, La Fleur M, Wood WI;

XX DR WPI: 2000-587437/55.

XX DR N-PSDB; AAA88515.

XX Novel PRO polypeptides useful for preventing or rescuing retinal cells from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, uveitis -

XX Claim 2; Fig 2; 140pp; English.

XX The present sequence is that of human PRO200 or vascular endothelial growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515) that was isolated from a glioma cell line G61 library using probes (see AAA8523-26) based on an expressed sequence tag (see AAA8522) that showed homology to VEGF. PRO200 has a predicted mol wt. of 39.029 and a pI of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, amacrine cells, displaced amacrine cells, horizontal and bipolar neurons, and supportive cells (including Muller cells and pigment epithelial cells) from injury and degradation. The retinal cells are preferably photoreceptors and photoreceptor cell injury or death is caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinitis pigmentosa, macular degeneration, including age-related, retinal detachment, retinal tears, retinopathy, retinal degenerative diseases, macular holes, degenerative myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or contusion such as Furtcher's retinopathy, edema, ischemic conditions such as central or branch retinal vision occlusion, collagen vascular diseases, thrombocytopenic purpura, uveitis, retinal vasculitis and occlusion associated with Eales

CC disease and systemic lupus erythematosus (claimed).

XX SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166; Indels 0; Gaps 0;

Matches 317; Conservative 0; Mismatches 0;

QY 2 KQFSSNKEQGVQDPQHERIITVTNGSIHSPRPFTYPRNTVLVRLVAVENVMQIOL 61

Db 29 KQFSSNKEQGVQDPQHERIITVTNGSIHSPRPFTYPRNTVLVRLVAVENVMQIOL 88

QY 62 TFDERFGLDEDDICKYDFVEVEBPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121

Db 89 TFDERFGLDEDDICKYDFVEVEBPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148

QY 122 YPSPGFCIHYNIVMPOFTEAVSPVLPSPALPDLLNNAITAFSTLEDLIRYLEPERW 181

Db 149 YPSPGFCIHYNIVMPOFTEAVSPVLPSPALPDLLNNAITAFSTLEDLIRYLEPERW 208

QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYCTPRNFSVSIREELKRTDT 241

Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYCTPRNFSVSIREELKRTDT 268

QY 242 IFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVLQIRPKTGVRLHKSITDVA 301

Db 269 IFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVLQIRPKTGVRLHKSITDVA 328

QY 302 LEHHEECDCVCRGSGTG 318

Db 329 LEHHEECDCVCRGSGTG 345

RESULT 14

AAAB33414

ID AAAB33414 standard; Protein; 345 AA.

XX AC AAAB33414;

XX DT 29-JAN-2001 (first entry)

XX DE Human PRO200 protein UNQ174 SEQ ID NO:2.

XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.

XX OS Homo sapiens.

XX WO200053758-A2.

XX PD 14-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05841.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 10-MAR-1999; 99US-0123618.

XX PR 12-MAR-1999; 99US-0123957.

XX PR 23-MAR-1999; 99US-0125775.

XX PR 12-APR-1999; 99US-0128849.

XX PR 20-APR-1999; 99WO-US08615.

XX PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 16-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabatoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;  
 DR WPI; 2000-572271/53.  
 DR N-PSDB; AAC58579.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 33; Fig 2; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 XX Sequence 345 AA;  
 XX  
 XX Query Match 99.7%; Score 1728; DB 21; Length 345;  
 XX Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 XX Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVQL 61  
 DB 29 KQFSSNKEQGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVQL 88  
 QY 62 TFDERFGLDEPDICKYDFVEVEEPSDGTILGWCSGTVPGKQISKGNQIRIRFVSDE 121  
 DB 89 TFDERFGLDEPDICKYDFVEVEEPSDGTILGWCSGTVPGKQISKGNQIRIRFVSDE 148  
 QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRVLEPERW 181  
 DB 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRVLEPERW 208  
 QY 182 QLDLEDLYRPTWQLLGKAFVGRKSRVVDLNLLEEVRLYSCCTPRNFSVSIREELKRTDT 241  
 DB 209 QLDLEDLYRPTWQLLGKAFVGRKSRVVDLNLLEEVRLYSCCTPRNFSVSIREELKRTDT 268  
 QY 242 IFWPGCLLVRCGNCACCLHNCNECQCVSKTKKTHEVLQLRPKTGVRGLHKS LTDVA 301  
 DB 269 IFWPGCLLVRCGNCACCLHNCNECQCVSKTKKTHEVLQLRPKTGVRGLHKS LTDVA 328  
 QY 302 LEHHECDVCVCRGSTGG 318  
 DB 329 LEHHECDVCVCRGSTGG 345

RESULT 15  
 AAB24412  
 ID AAB24412 standard; Protein; 345 AA.  
 XX  
 AC AAB24412;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO713 protein sequence SEQ ID NO:137.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cytosstatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 XX Watanabe CK, Williams PM, Wood WI;



```
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77621.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating disorders in mammals -
XX angio-genic disorders in mammals -
XX
PS Claim 72; Fig 50; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating disorders in mammals by
CC cardiovascular, endothelial or angio-genic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angio-genic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 345 AA;
Query Match 99.7%; Score 1728; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 61
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 88
QY 62 TFDERFGLDPEDDICKYDFVEVEPSDGTILGRWCGSTVPGKQISKGNQIRIRFVSDE 121
DB 89 TFDERFGLDPEDDICKYDFVEVEPSDGTILGRWCGSTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIVMPQTEAVSPSVLPFSAFLDLNNAITAFSTLEDLIRYLEPERW 181
DB 149 YFPSEPGFCIHYNIVMPQTEAVSPSVLPFSAFLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTVEVRLYSCTPRNFSVSIRELKETDT 241
DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTVEVRLYSCTPRNFSVSIRELKETDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKYHVLQLRPKTVGRGLHKS LTDVA 301
DB 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKYHVLQLRPKTVGRGLHKS LTDVA 328
QY 302 LEHHECDCVCRGSTGG 318
DB 329 LEHHECDCVCRGSTGG 345
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Search completed: November 25, 2003, 21:02:14  
Job time : 34.125 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:00:19 ; Search time 11.9881 Seconds  
(without alignments)  
1122.351 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GKQFQSNKEQGVQDPQHE.....DVALEHHECDVCVRGSGTG 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1728	99.7	345	4	US-09-040-220D-2
2	1728	99.7	345	4	US-09-457-066-2
3	1728	99.7	345	4	US-09-265-686-2
4	1728	99.7	345	4	US-09-540-224-5
5	1728	99.7	345	4	US-09-564-595D-33
6	1728	99.7	345	4	US-09-706-968-2
7	1559	89.9	345	4	US-09-457-066-43
8	1559	89.9	345	4	US-09-564-595D-35
9	1559	89.9	345	4	US-09-706-968-43
10	1325	76.4	302	4	US-09-564-595D-54
11	1266.5	73.0	303	4	US-09-564-595D-57
12	1098	63.3	316	4	US-09-564-595D-55
13	1051.5	60.6	317	4	US-09-564-595D-56
14	741	42.7	370	4	US-09-457-066-37
15	741	42.7	370	4	US-09-540-224-2
16	741	42.7	370	4	US-09-564-595D-2
17	741	42.7	370	4	US-09-706-968-37
18	736	42.4	370	4	US-09-540-224-4
19	736	42.4	370	4	US-09-564-595D-53
20	172.5	9.9	730	3	US-08-872-757-2
21	172.5	9.9	730	3	US-09-850-048A-2
22	172	9.9	1012	4	US-08-285-385C-4
23	171	9.9	1015	4	US-09-285-385C-2
24	169	9.7	788	1	US-08-572-225-1
25	169	9.7	986	4	US-09-285-385C-19
26	165	9.5	3623	4	US-09-341-461-2
27	163.5	9.4	909	3	US-08-936-135-18

28	163.5	9.4	922	4	US-09-116-473-4	Sequence 4, Appli
29	163.5	9.4	926	3	US-08-936-135-20	Sequence 20, Appli
30	163	9.4	101	3	US-09-374-135-6	Sequence 6, Appli
31	163	9.4	925	4	US-09-116-473-2	Sequence 2, Appli
32	160.5	9.3	923	3	US-08-936-135-6	Sequence 6, Appli
33	159.5	9.2	901	3	US-08-936-135-22	Sequence 22, Appli
34	159.5	9.2	906	3	US-08-936-135-24	Sequence 24, Appli
35	159.5	9.2	909	3	US-08-936-135-8	Sequence 8, Appli
36	159.5	9.2	909	3	US-08-936-135-10	Sequence 10, Appli
37	159.5	9.2	914	3	US-08-936-135-12	Sequence 12, Appli
38	159.5	9.2	926	3	US-08-936-135-14	Sequence 14, Appli
39	159.5	9.2	931	3	US-08-936-135-16	Sequence 16, Appli
40	158.5	9.1	111	4	US-09-341-461-30	Sequence 30, Appli
41	156	9.0	986	3	US-08-872-757-4	Sequence 4, Appli
42	156	9.0	986	4	US-09-850-048A-4	Sequence 4, Appli
43	154	8.9	449	2	US-08-839-008-2	Sequence 2, Appli
44	154	8.9	449	2	US-08-839-008-9	Sequence 9, Appli
45	153	8.8	415	3	US-09-032-523-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-040-220D-2

; Sequence 2, Application US/09040220D

; Patent No. 6391311

; GENERAL INFORMATION:

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Kuo, Sophia S.

; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC

; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,

; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION

; FILE REFERENCE: P1122

; CURRENT APPLICATION NUMBER: US/09/040.220D

; CURRENT FILING DATE: 1998-03-17

; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 2

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Human

US-09-040-220D-2

Query Match	99.7%	Score 1728;	DB 4;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 2.1e-179;	Mismatches 0;	Gaps 0;
Matches 317;	Conservative 0;			
Qy	2	KQFSSNKEQGVQDPQHE	IIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVTQL	61
Db	29	KQFSSNKEQGVQDPQHE	IIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVTQL	88
Qy	62	TFPERFGLPEPDDICKYDFVEVEEPPSDGILGRWCSSGVTPGKQISKGNQIRIRFVSDE	121	
Db	89	TFPERFGLPEPDDICKYDFVEVEEPPSDGILGRWCSSGVTPGKQISKGNQIRIRFVSDE	148	
Qy	122	YFPSEPGFCHYINVMQFTEAVSPVLPSPALPLDNLNNAITAFSTLEDLIRVLEPERW	181	
Db	149	YFPSEPGFCHYINVMQFTEAVSPVLPSPALPLDNLNNAITAFSTLEDLIRVLEPERW	208	
Qy	182	QLDLEDLIRFTWQLLGKAFVFGKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIRESLKRKTD	241	
Db	209	QLDLEDLIRFTWQLLGKAFVFGKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIRESLKRKTD	268	
Qy	242	IFWPGCLLVKRCGNCACCLHNCNQCQVPSKVTKKYKTHEVLQLRPKTGVGLHKSLLTDA	301	
Db	269	IFWPGCLLVKRCGNCACCLHNCNQCQVPSKVTKKYKTHEVLQLRPKTGVGLHKSLLTDA	328	
Qy	302	LEHHERCDVCVRGSGTG	318	
Db	329	LEHHERCDVCVRGSGTG	345	

```
RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; NUMBER FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match
Best Local Similarity 99.7%; Score 1728; DB 4; Length 345;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db 29 KQFSSNKEQGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy 62 TFDERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148
Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 328
Qy 302 LEHHEECDCVCRGSTGG 318
Db 329 LEHHEECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match
Best Local Similarity 99.7%; Score 1728; DB 4; Length 345;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db 29 KQFSSNKEQGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy 62 TFDERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148
Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268

RESULT 3
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: F1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Human
US-09-265-686-2

Query Match
Best Local Similarity 99.7%; Score 1728; DB 4; Length 345;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db 29 KQFSSNKEQGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy 62 TFDERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148
Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268
```

QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSLLTDA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSLLTDA 328  
QY 302 LEHHECDCVCRGSTG 318  
Db 329 LEHHECDCVCRGSTG 345

## RESULT 5

US-09-564-595D-33  
; Sequence 33, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-564-595D-33

Query Match 99.7%; Score 1728; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.1e-179;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL 88  
QY 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148  
QY 122 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSIRBELKRTDT 241  
Db 209 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSLLTDA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSLLTDA 328  
QY 302 LEHHECDCVCRGSTG 318  
Db 329 LEHHECDCVCRGSTG 345

## RESULT 6

US-09-706-968-2  
; Sequence 2, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-706-968-2

Query Match 99.7%; Score 1728; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.1e-179;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL 88  
QY 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148  
QY 122 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSIRBELKRTDT 241  
Db 209 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSLLTDA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRLHKSLLTDA 328  
QY 302 LEHHECDCVCRGSTG 318  
Db 329 LEHHECDCVCRGSTG 345

## RESULT 7

US-09-457-066-43  
; Sequence 43, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-457-066-43

Query Match 89.9%; Score 1559; DB 4; Length 345;  
Best Local Similarity 87.3%; Pred. No. 4.9e-161;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

Qy 2 KFPSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61  
Db 29 KLQSSDKEQNGVODPRHERVVTISNGSIHSPKFPHTYPRNMLVWRLVAEENVMQIOL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPESDGTILGRCGSGTVPGKQISKGNIQIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPESDGTILGRCGSGTVPGKQISKGNIQIRFVSDE 148  
Qy 122 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QVLDLSLYKPTWQLLKGAFVGRKSKVNVNLLKEEVKLYSCTPRNFSVSIREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRGLHKS LTDVA 328  
Qy 302 LEHHEECDCVCRGSGTG 318  
Db 329 LEHHEECDCVCRGSGTG 345

## RESULT 8

US-09-564-595D-35  
; Sequence 35, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-564-595D-35

Query Match 89.9%; Score 1559; DB 4; Length 345;  
Best Local Similarity 87.1%; Pred. No. 4.9e-161;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 KFPSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61  
Db 29 KLQSSDKEQNGVODPRHERVVTISNGSIHSPKFPHTYPRNMLVWRLVAEENVMQIOL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPESDGTILGRCGSGTVPGKQISKGNIQIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPESDGTILGRCGSGTVPGKQISKGNIQIRFVSDE 148  
Qy 122 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QVLDLSLYKPTWQLLKGAFVGRKSKVNVNLLKEEVKLYSCTPRNFSVSIREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRGLHKS LTDVA 328  
Qy 302 LEHHEECDCVCRGSGTG 318  
Db 329 LEHHEECDCVCRGSGTG 345

Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRGLHKS LTDVA 328  
Qy 302 LEHHEECDCVCRGSGTG 318  
Db 329 LEHHEECDCVCRGSGTG 345  
RESULT 9  
US-09-706-968-43  
; Sequence 43, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-706-968-43

Query Match 89.9%; Score 1559; DB 4; Length 345;  
Best Local Similarity 87.1%; Pred. No. 4.9e-161;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 KFPSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61  
Db 29 KLQSSDKEQNGVODPRHERVVTISNGSIHSPKFPHTYPRNMLVWRLVAEENVMQIOL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPESDGTILGRCGSGTVPGKQISKGNIQIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPESDGTILGRCGSGTVPGKQISKGNIQIRFVSDE 148  
Qy 122 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QVLDLSLYKPTWQLLKGAFVGRKSKVNVNLLKEEVKLYSCTPRNFSVSIREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRGLHKS LTDVA 328  
Qy 302 LEHHEECDCVCRGSGTG 318  
Db 329 LEHHEECDCVCRGSGTG 345

## RESULT 10

US-09-564-595D-54  
; Sequence 54, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19

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; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

Query Match          76.4%; Score 1325; DB 4; Length 302;
Best Local Similarity 82.8%; Pred. No. 1.1e-135;
Matches 246; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

Qy 19 HERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMWLTDFRFGLEDPEDDICK 78
Db 1 HERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMWLTDFRFGLEDPEDDICK 60

Qy 79 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHYNVMP 138
Db 61 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHYNVMP 120

Qy 139 QFTEAVSPVLPPSALPLDLNNATAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 198
Db 121 QFTEAVSPVLPPSALPLDLNNATAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 180

Qy 199 AFVFGKRSRVVDLMLLNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 258
Db 181 AFVFGKRSRVVDLMLLNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 239

Qy 259 CCLHNCNECQCVSKVTKYHEVLQRLP---KTGVRGLHSLTDVALEHHEECDCVC 312
Db 240 CGTVNRSCTCNSGKTVKTKYHEVLQRLPFGHKKRGRKTKWALVDIQLDHERCDCIC 296

RESULT 11
US-09-564-595D-57
; Sequence 57, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57

Query Match          73.0%; Score 1266.5; DB 4; Length 303;
Best Local Similarity 78.9%; Pred. No. 2.6e-129;
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Matches 240; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

Qy 20 ERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMWLTDFRFGLEDPEDDICK 79
Db 2 DETIQKNGYVQSPRPNSYPRNLLTLWRLHS-QENTRIQLVFDNQGLSEANDICRY 60

Qy 80 DFEVEEPSDGT--ILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHYNVMP 137
Db 61 DFEVEDISSETTIIRGRWCGHKEVPPRIKSRNTQKITFKSDDYFVAKPGFKIYSL-L 119

Qy 138 PQFTEA---VSPSVLPPSALPLDLNNATAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 194
Db 120 EDFQAAASVSPVLPPSALPLDLNNATAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 179

Qy 195 LLGKAFVFGKRSRVVDLMLLNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 254
Db 180 LLGKAFVFGKRSRVVDLMLLNTAFSTLEDLIRYLEPERWQDLEDLYRPTWQ 239

Qy 255 GNCACCLHNCNECQCVSKVTKYHEVLQRLP---KTGVRGLHSLTDVALEHHEECDCVC 314
Db 240 GNCACCLHNCNECQCVSKVTKYHEVLQRLP---KTGVRGLHSLTDVALEHHEECDCVC 299

Qy 315 STGG 318
Db 300 STGG 303

RESULT 12
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match          63.3%; Score 1098; DB 4; Length 316;
Best Local Similarity 67.1%; Pred. No. 5.7e-111;
Matches 210; Conservative 26; Mismatches 55; Indels 22; Gaps 5;

Qy 19 HERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMWLTDFRFGLEDPEDDICK 78
Db 1 HERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMWLTDFRFGLEDPEDDICK 60

Qy 79 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHYNVMP 138
Db 61 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHYNVMP 120

Qy 139 QFTEAV-----SPSVLPPSALPLDLNNATAFSTLEDLIRYLEPERWQ 182
Db 121 QFTEAVTNSVTSSIGSVNSPSTVDTPT-LIADALDKKIAEDFTVDDLKYNFESWQ 179

Qy 183 LDLEDLYRPTWQLGKAFVFGKRSRVVDLMLLNTAFSTLEDLIRYLEPERWQ 242
Db 183 LDLEDLYRPTWQLGKAFVFGKRSRVVDLMLLNTAFSTLEDLIRYLEPERWQ 242
```

```
Db 180 EDLENMYLDTPRYGRSY-HDRKSK-VDLRLNDADAKRYSCTPRNYSVNIREEKLNAVY 237
Qy 243 FWPGLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRP---KTGVRGLHKS LTD 299
Db 238 FFPFCLLVKRCGNCAGGTNNWRSCTNSKTKYKHYHEVLQFEPGCHKRRGRKTAHWALVD 297
Qy 300 VALEHHEECDCVC 312
Db 298 IQLDHERCDDIC 310

RESULT 13
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match 60.6%; Score 1051.5; DB 4; Length 317;
Best Local Similarity 63.8%; Pred. No. 6.5e-106;
Matches 204; Conservative 36; Mismatches 55; Indels 25; Gaps 6;

Qy 20 ERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVIQLTFDERFGLEDPEDDICKY 79
Db 2 DETIQKGVGVQSPRPFPNSYPRNLLTWRLHS-QENTRIQLVFDNQGLEAENDICRY 60
Qy 80 DFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDYFSEPGFCIHNYVM 137
Db 61 DFVEVEDISSTIIRGRWGHKEVPPRIKSRNQIKITFRSDDYFVAKPGFKIYVSL-L 119
Qy 138 PQTEAV-----SPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEP 178
Db 120 EDFQAAASSETNWESVTSSISGVSNPSVTDPT-LIADALDKKIAEFDVEDLLKYFNP 178
Qy 179 ERQWLDLEDYRPTWQLLGAFFGKRSRVVDNLNLTVEEVRVLYSCTPRNFSVIRELKR 238
Db 179 ESWQEDLENMILDTPRYGRSY-HDRKSKVVDNLNLTVEEVRVLYSCTPRNFSVIRELKR 237
Qy 239 TDIFWPGCLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRPKTGVRGLHKS LTD 298
Db 238 TDIFWPGCLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRPKTGVRGLHKS LTD 297
Qy 299 DVALEHHEECDCVCRGSGTG 318
Db 298 DVALEHHEECDCVCRGSGTG 317

RESULT 14
US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-37

Query Match 42.7%; Score 741; DB 4; Length 370;
Best Local Similarity 46.6%; Pred. No. 4.7e-72;
Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;

Qy 10 EQNGVQD-POHERIIVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVIQLTFDERFG 68
Db 42 ESNHLDLYRDETIOVKGNGYVQSPFPNSYPRNLLTWRLHS-QENTRIQLVFDNQFG 100
Qy 69 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDYFSE 126
Db 101 LEEAENDICRYDFVEVEDISSTIIRGRWGHKEVPPRIKSRNQIKITFRSDDYFVAK 160
Qy 127 PGFCIHNYVMQFTEAV-----SPSVLPSPSALPLDLNNAITAFS 167
Db 161 PGFKIYVSL-LEDQFQAAASSETNWESVTSSISGVSNPSVTDPT-LIADALDKKIAEFD 218
Qy 168 TLEDLRYLEPERWQDLEDLYRPTWQLLGAFFGKRSRVVDNLNLTVEEVRVLYSCTPRN 227
Db 219 TVEDLLKYFNPESWQEDLENMILDTPRYGRSY-HDRKSK-VDLRLNDADAKRYSCTPRN 276
Qy 228 FSVSIREELARTDTIFWPGCLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRP- 286
Db 277 YSVNIREEKLNAVVPFRCLLVQRCGNGCGGTNNWRSCTNSGKTKYKHYHEVLQFEPG 336

RESULT 15
US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match 42.7%; Score 741; DB 4; Length 370;
Best Local Similarity 46.6%; Pred. No. 4.7e-72;
Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;
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Qy	10	BONGVOD--PQHERITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIOLTDFDRPG	68
Db	42	ESNHLTDIYRRDETIOVKXNGVQSPRPNSYPRNLLTWRUHS--QENRIQLVFDNQFG	100
Qy	69	LEDPEDDICKDFVEVEBPSDGT--ILGRWCSSGTVPGQISKGNQIRIRFVSDEYFPSE	126
Db	101	LEEAENDICRYDFVEVEDISETSTIIRGWCGHKEVPPRIKSRWQIKITFKSDDDYFVAK	160
Qy	127	PGFCIHYNVMPQFTEAV-----SPSVLPSPSALPLDLNNAITAPS	167
Db	161	PGFKIYLSL-LDFDOPAAASETNWBSVTSSISGVYNPSFVDTPT-LTADALDKXIAEED	218
Qy	168	TLEDILRYLEPERWQOLDLEDLYRPTWQLIGKAFVCRKSRVVDLNLITBEVRLSYCTPN	227
Db	219	TVEDLLKYFNPESMQCEDLNNMYLDPTRYKGRSY-HDRKSK-VDLDRLNDDAKRYSTCPN	276
Qy	228	FSVSTIREELKRTDITFWPGCLLVKECGGNACCLHNCNECQVPKTVKXHYEVLQLRP-	286
Db	277	YSVNWIREELKANVFFPRCLLVQRCGGNCGGTVNRWRSCTNSGKTVKXHYEVLQFEFG	336
Qy	287	--KTGVRGLHKSLLTDVALEHHEECDCVC	312
Db	337	HIKRGRAKTWALVDIQLDHIERCDCIC	364

Search completed: November 25, 2003, 21:06:21  
Job time : 12.9881 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:04:39 ; Search time 22.3988 Seconds  
(without alignments)  
2618.575 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score:

Sequence: 1 GKQFSSNKEQNGVQDPQHE.....DVALEHHEECDVCRGSTGG 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 segs. 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Minimum DB seq length:	0
Maximum DB seq length:	2000000000

Post-processing: Minimum Match 08

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- Full Name Applications: PA:
- |     |  |
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| 1:  | /cgn2_6/pdata1/1/pubpaa/US07_PUBCOMB.pcp:  |
| 2:  | /cgn2_6/pdata1/1/pubpaa/PCT_NEW_PUB.pcp:   |
| 3:  | /cgn2_6/pdata1/1/pubpaa/US06_NEW_PUB.pcp:  |
| 4:  | /cgn2_6/pdata1/1/pubpaa/US06_PUBCOMB.pcp:  |
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| 7:  | /cgn2_6/pdata1/1/pubpaa/US08_NEW_PUB.pcp:  |
| 8:  | /cgn2_6/pdata1/1/pubpaa/US09_PUBCOMB.pcp:  |
| 9:  | /cgn2_6/pdata1/1/pubpaa/US09A_PUBCOMB.pcp: |
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| 11: | /cgn2_6/pdata1/1/pubpaa/US09C_PUBCOMB.pcp: |
| 12: | /cgn2_6/pdata1/1/pubpaa/US09_NEW_PUB.pcp:  |
| 13: | /cgn2_6/pdata1/1/pubpaa/US10A_PUBCOMB.pcp: |
| 14: | /cgn2_6/pdata1/1/pubpaa/US10B_PUBCOMB.pcp: |
| 15: | /cgn2_6/pdata1/1/pubpaa/US10C_PUBCOMB.pcp: |
| 16: | /cgn2_6/pdata1/1/pubpaa/US10_NEW_PUB.pcp:  |
| 17: | /cgn2_6/pdata1/1/pubpaa/US60_NEW_PUB.pcp:  |
| 18: | /cgn2_6/pdata1/1/pubpaa/US60_PUBCOMB.pcp:  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query %			Description		
	Score	Match	Length	DB	ID	
1	1734	100.0	318	10	US-09-852-209A-5	Sequence 5, Appli
2	1734	100.0	318	15	US-10-131-600-5	Sequence 5, Appli
3	1728	99.7	345	9	US-09-823-033-2	Sequence 2, Appli
4	1728	99.7	345	9	US-09-818-943-1	Sequence 1, Appli
5	1728	99.7	345	9	US-09-923-935-4	Sequence 4, Appli
6	1728	99.7	345	10	US-09-923-006A-149	Sequence 149, App
7	1728	99.7	345	10	US-09-978-295A-488	Sequence 488, App
8	1728	99.7	345	10	US-09-852-209A-3	Sequence 3, Appli
9	1728	99.7	345	10	US-09-852-209A-3	Sequence 488, App
10	1728	99.7	345	10	US-09-978-192A-488	Sequence 488, App
11	1728	99.7	345	10	US-09-959-832A-488	Sequence 488, App
12	1728	99.7	345	11	US-09-978-189-488	Sequence 488, App
13	1728	99.7	345	11	US-09-796-753-6	Sequence 6, Appli
14	1728	99.7	345	11	US-09-978-608A-488	Sequence 488, App
15	1728	99.7	345	11	US-09-978-585A-488	Sequence 488, App

Query Match	100.0%	Score 1734	DB 10	Length 318
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Best Local Similarity 100.0%; Pred. No. 1.2e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60

61 LTFDERFGLDPEDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
61 LTFDERFGLDPEDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 120

121 EYFSPGFCIHYNIVMPOFTAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180  
121 EYFSPGFCIHYNIVMPOFTAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180

181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTD 240  
181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTD 240

241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDV 300  
241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDV 300

301 ALEHHECDCVCRGSTGG 318  
301 ALEHHECDCVCRGSTGG 318

## RESULT 2

US-10-131-600-5  
; Sequence 5, Application US/10131600  
; Publication No. US20030082670A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Karli  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOUTZ, Christen  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10/131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-600-5

Query Match 100.0%; Score 1734; DB 15; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.2e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60

Db 1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
Qy 61 LTFDERFGLDPEDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
Db 61 LTFDERFGLDPEDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
Qy 121 EYFSPGFCIHYNIVMPOFTAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180  
Db 121 EYFSPGFCIHYNIVMPOFTAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180  
Qy 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTD 240  
Db 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTD 240  
Qy 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDV 300  
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDV 300  
Qy 301 ALEHHECDCVCRGSTGG 318  
Db 301 ALEHHECDCVCRGSTGG 318

## RESULT 3

US-09-823-033-2  
; Sequence 2, Application US/09823033  
; Patent No. US20020004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 99.7%; Score 1728; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 88  
Qy 62 TDFERFGLDPEDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 121  
Db 89 TDFERFGLDPEDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 148  
Qy 122 YFSPGFCIHYNIVMPOFTAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 181  
Db 149 YFSPGFCIHYNIVMPOFTAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 208  
Qy 182 QDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTD 241  
Db 209 QDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTD 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDV 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDV 328  
Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345

## RESULT 4

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US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-943-1

Query Match      99.7%; Score 1728; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KFOFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVLIQL 61
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Qy  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 6
US-09-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-149

Query Match      99.7%; Score 1728; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KFOFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVLIQL 61
Db  29 KFOFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVLIQL 88
Qy  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
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US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-943-1

Query Match      99.7%; Score 1728; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KFOFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVLIQL 61
Db  29 KFOFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVLIQL 88
Qy  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 5
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 2001-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4
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QY      302  LEHHEBCDCVCRGSTGG 318
Db      329  LEHHEBCDCVCRGSTGG 345

RESULT 7
US-09-978-295A-488
; Sequence 488, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Eilen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
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; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
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Db	89	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD	14
Qy	122	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW	181
Db	149	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW	208
Qy	182	OLDLEDLYRETWQILGKAFVGRKSRVVDNLNLTTEVRVLYSCTTPRNFVSISREELKRTDT	241
Db	209	OLDLEDLYRETWQILGKAFVGRKSRVVDNLNLTTEVRVLYSCTTPRNFVSISREELKRTDT	268
Qy	242	IFWPGCLLVKRCGNCACCLHNCNECQCVPFSKVTKKYKHEVQLRPTKTVGRGLHKSJTDVA	301
Db	269	IFWPGCLLVKRCGNCACCLHNCNECQCVPFSKVTKKYKHEVQLRPTKTVGRGLHKSJTDVA	328
Qy	302	LEHHECDCVCRGSTGG 318	
Db	329	LEHHECDCVCRGSTGG 345	
RESULT 8			
US-09-852-209A-3			
; Sequence 3, Application US/09852209A			
; Patent No. US20020164687A1			
; GENERAL INFORMATION:			
; APPLICANT: ERIKSSON, Ulf			
; APPLICANT: AASE, Karin			
; APPLICANT: LEE, Xuri			
; APPLICANT: PONTEN, Annica			
; APPLICANT: UUTELA, Marko			
; APPLICANT: ALITALO, Kari			
; APPLICANT: OESTMAN, Arne			
; APPLICANT: HELDIN, Carl-Henrik			
; APPLICANT: BETSHOLTZ, Christer			
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING			
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740			
; CURRENT APPLICATION NUMBER: US/09/852,209A			
; CURRENT FILING DATE: 2001-05-10			
; PRIOR APPLICATION NUMBER: 09/410,349			
; PRIOR FILING DATE: 1999-09-30			
; PRIOR APPLICATION NUMBER: 60/110,749			
; PRIOR FILING DATE: 1998-12-03			
; PRIOR APPLICATION NUMBER: 60/113,002			
; PRIOR FILING DATE: 1998-12-18			
; PRIOR APPLICATION NUMBER: 60/135,426			
; PRIOR FILING DATE: 1999-05-21			
; PRIOR APPLICATION NUMBER: 60/144,022			
; PRIOR FILING DATE: 1999-07-15			
; NUMBER OF SEQ ID NOS: 39			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 345			
; TYPE: PRM			
; ORGANISM: Homo sapiens			
US-09-852-209A-3			
Query Match 99.7%; Score 1728; DB 10; Length 345;			
Best Local Similarity 100.0%; Pred. No. 5.3e-166;			
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL 61	
Db	29	KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL 88	
Qy	62	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD	121
Db	89	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD	148
Qy	122	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW	181
Db	149	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW	208









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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.7%; Score 1728; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPFRFPHYPRNTVLVWRLVAEENWVQL 61
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPFRFPHYPRNTVLVWRLVAEENWVQL 88
QY 62 TDEREGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121
DB 89 TDEREGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148
QY 122 YPSEPGFCIHYNVMPQTEAVSPVLPSALPLDLNNAITAFSTLRLHYLSPERW 181
DB 149 YPSEPGFCIHYNVMPQTEAVSPVLPSALPLDLNNAITAFSTLRLHYLSPERW 208
QY 182 QLDLEDLYPTWQLLGAFAVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 241
DB 209 QLDLEDLYPTWQLLGAFAVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKTKKYHEVLQRPKTVGRGLHKSITDVA 301
DB 269 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKTKKYHEVLQRPKTVGRGLHKSITDVA 328
QY 302 LEHHEECDCVCRGSTGG 318
DB 329 LEHHEECDCVCRGSTGG 345
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RESULT 11
US-09-999-832A-488
; Sequence 488, Application US/099999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
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; PRIOR APPLICATION NUMBER: 60/081838  
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; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
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; PRIOR APPLICATION NUMBER: 60/083495  
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; PRIOR APPLICATION NUMBER: 60/083496  
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; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
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; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
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; PRIOR FILING DATE: 1998-05-07  
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; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07

;  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
;  
Query Match 99.7%; Score 1728; DB 10; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
Qy 2 KQFSSNKEQGVDDPOHERITVTSTNGSIHSPRFHTYPRNTVLVRLVAEENWVQL 61  
Db 29 KQFSSNKEQGVDDPOHERITVTSTNGSIHSPRFHTYPRNTVLVRLVAEENWVQL 88  
;  
Qy 62 TPDREGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRFVSDE 121  
Db 89 TPDREGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRFVSDE 148  
;  
Qy 122 YFPSEPGFCIHYNVMPQTEAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLBPERW 181  
Db 149 YFPSEPGFCIHYNVMPQTEAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLBPERW 208  
;  
Qy 182 QLDLEDLYEPTWQLLGKAFVFGKSRVVDNLNLTTEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QLDLEDLYEPTWQLLGKAFVFGKSRVVDNLNLTTEVRVLYSCTPRNFSVSIREELKRTDT 268  
;  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKS LTDVA 328  
;  
Qy 302 LEHHERCDCVCRGSTGG 318  
Db 329 LEHHERCDCVCRGSTGG 345  
;  
RESULT 12  
US-09-978-189-488  
; Sequence 488, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR APPLICATION NUMBER: 60/081955  
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PRIOR APPLICATION NUMBER: 60/082568  
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PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441

FILE REFERENCE: 7853-227-999  
CURRENT APPLICATION NUMBER: US/09/796,753  
CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 09/183,175  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 09/223,094  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/223,546  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/224,246  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/259,388  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/122,458  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: 09/312,359  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/336,536  
PRIOR FILING DATE: 1999-06-18  
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PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 09/345,464  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/365,164  
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PRIOR FILING DATE: 1999-12-23  
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PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/474,072  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/514,010  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 09/516,745  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 09/572,002  
PRIOR FILING DATE: 2000-05-14  
PRIOR APPLICATION NUMBER: 09/597,993  
PRIOR FILING DATE: 2000-06-19  
PRIOR APPLICATION NUMBER: 09/599,596  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 09/630,334  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: 09/606,565  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/606,317  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/665,666  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: 09/677,751  
PRIOR FILING DATE: 2000-09-30  
NUMBER OF SEQ ID NOS: 162  
SEQ ID NO 6  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-796-753-6

Query Match 99.7%; Score 1728; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 61  
DB 29 KQFSSNKEQGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 88  
QY 62 TFDERFGLDEDDICKYDFVEVEEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121  
DB 89 TFDERFGLDEDDICKYDFVEVEEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 148  
QY 122 YFPSPGFCIHNIWMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSPGFCIHNIWMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWLLGKAFVFGKRSVVDNLNLTTEVRVLYSCTPRNFSVSIREEKRTDT 241  
DB 209 QLDLEDLYRPTWLLGKAFVFGKRSVVDNLNLTTEVRVLYSCTPRNFSVSIREEKRTDT 268  
QY 242 IFWPGLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTVGRGLHKSITDVA 301  
DB 269 IFWPGLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTVGRGLHKSITDVA 328  
QY 302 LEHHEEDCVCRGSTGG 318  
DB 329 LEHHEEDCVCRGSTGG 345

RESULT 13  
US-09-796-753-6  
Sequence 6, Application US/09796753  
Publication No. US20030027998A1  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

Query Match 99.7%; Score 1728; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 61  
DB 29 KQFSSNKEQGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 88  
QY 62 TFDERFGLDEDDICKYDFVEVEEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121  
DB 89 TFDERFGLDEDDICKYDFVEVEEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 148

QY 122 YFPSEPGFCIHYNVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 DB 149 YFPSEPGFCIHYNVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
 QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDT 241  
 DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDT 268  
 QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSPKTKYHVLQRPKTGVRGLHKS LTDVA 301  
 DB 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSPKTKYHVLQRPKTGVRGLHKS LTDVA 328  
 QY 302 LEHHEBCDCVCRGSTGG 318  
 DB 329 LEHHEBCDCVCRGSTGG 345

## RESULT 14

US-09-978-608A-488  
 ; Sequence 488, Application US/09978608A  
 ; Publication No. US20030045462A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC22

; CURRENT APPLICATION NUMBER: US/09/978,608A

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 488

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-608A-488

Query Match 99.7%; Score 1728; DB 11; Length 345;

Best Local Similarity 100.0%; Pred. No. 5.3e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAVENWVQL 61

DB 29 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAVENWVQL 88

QY 62 TFERFGLPEDDICKYDFVEVEPSDGTILGRWCGSGTVPKGQISKGNOIRIRFVSDE 121

DB 89 TFERFGLPEDDICKYDFVEVEPSDGTILGRWCGSGTVPKGQISKGNOIRIRFVSDE 148  
 QY 122 YFPSEPGFCIHYNVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 DB 149 YFPSEPGFCIHYNVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
 QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDT 241  
 DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDT 268  
 QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSPKTKYHVLQRPKTGVRGLHKS LTDVA 301  
 DB 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSPKTKYHVLQRPKTGVRGLHKS LTDVA 328  
 QY 302 LEHHEBCDCVCRGSTGG 318  
 DB 329 LEHHEBCDCVCRGSTGG 345

## RESULT 15

US-09-978-585A-488

; Sequence 488, Application US/09978585A

; Publication No. US20030049633A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC15

; CURRENT APPLICATION NUMBER: US/09/978,585A

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 488

; LENGTH: 345

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-585A-488

Query Match 99.7%; Score 1728; DB 11; Length 345;

Best Local Similarity 100.0%; Pred. No. 5.3e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAVENWVQL 61

DB 29 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAVENWVQL 88

QY 62 TFERFGLPEDDICKYDFVEVEPSDGTILGRWCGSGTVPKGQISKGNOIRIRFVSDE 121



Db	89	TFDERGLEDPEDDICKYDFVEVEEFGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE	148
QY	122	YFSEFQFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW	181
Db	149	YFSEFQFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW	208
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Db	209	QLDLEDLYRPTWOLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT	268
QY	242	IFWPGCLLVKRCGNCACCLHNCNECQVPSKVKYHEVQLRPKTGVRGLHKS LTDVA	301
Db	269	IFWPGCLLVKRCGNCACCLHNCNECQVPSKVKYHEVQLRPKTGVRGLHKS LTDVA	328
QY	302	LEHHECDCVCRGSTGG	318
Db	329	LEHHECDCVCRGSTGG	345

Search completed: November 25, 2003, 21:17:05  
Job time : 23.3988 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:19 ; Search time 156.161 Seconds  
(without alignments)  
1852.926 Million cell updates/sec

Title: US-09-852-209A-5  
Perfect score: 1734  
Sequence: 1 GKFQSSNKEQGVDPQHE.....DVALEHHECDVCVRGSGG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main:\*

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32: /cgn2\_6/ptodata/1/paa/US60 COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1734	100.0	318	18	US-09-410-349A-5	Sequence 5, Appli
3	1734	100.0	318	23	US-09-852-209-5	Sequence 5, Appli
4	1734	100.0	318	23	US-09-852-209A-5	Sequence 5, Appli
5	1734	100.0	318	27	US-10-131-600-5	Sequence 5, Appli
6	1734	100.0	318	29	US-10-303-997B-5	Sequence 5, Appli
7	1728	99.7	323	1	PCT-US99-31025-29	Sequence 29, Appli
8	1728	99.7	345	18	US-09-471-179-29	Sequence 29, Appli
9	1728	99.7	345	1	PCT-US01-43523-286	Sequence 286, App
10	1728	99.7	345	1	PCT-US02-24563-286	Sequence 34, Appl
11	1728	99.7	345	1	PCT-US03-04213-34	Sequence 2, Appli
12	1728	99.7	345	1	PCT-US99-01574-2	Sequence 4, Appli
13	1728	99.7	345	1	PCT-US99-15783-4	Sequence 2, Appli
14	1728	99.7	345	1	PCT-US99-22668-3	Sequence 3, Appli
15	1728	99.7	345	1	PCT-US99-31025-2	Sequence 2, Appli
16	1728	99.7	345	15	US-09-184-216-2	Sequence 2, Appli
17	1728	99.7	345	16	US-09-207-120-2	Sequence 2, Appli
18	1728	99.7	345	16	US-09-223-546-2	Sequence 2, Appli
19	1728	99.7	345	16	US-09-237-705-2	Sequence 2, Appli
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21	1728	99.7	345	17	US-09-304-216-33	Sequence 33, Appli
22	1728	99.7	345	17	US-09-380-138-488	Sequence 488, App
23	1728	99.7	345	18	US-09-410-349A-3	Sequence 4, Appli
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25	1728	99.7	345	18	US-09-471-173-2	Sequence 2, Appli
26	1728	99.7	345	19	US-09-540-703-2	Sequence 2, Appli
27	1728	99.7	345	19	US-09-541-752-2	Sequence 2, Appli
28	1728	99.7	345	19	US-09-599-596-2	Sequence 2, Appli
29	1728	99.7	345	20	US-09-663-783-24	Sequence 24, Appl
30	1728	99.7	345	20	US-09-685-310-24	Sequence 24, Appl
31	1728	99.7	345	20	US-09-688-312-51	Sequence 51, Appl
32	1728	99.7	345	20	US-09-691-200-32	Sequence 32, Appl
33	1728	99.7	345	20	US-09-695-121-2	Sequence 2, Appli
34	1728	99.7	345	21	US-09-723-749-2	Sequence 2, Appli
35	1728	99.7	345	21	US-09-795-006A-149	Sequence 149, App
36	1728	99.7	345	22	US-09-796-753-6	Sequence 6, Appli
37	1728	99.7	345	23	US-09-818-943-1	Sequence 1, Appli
38	1728	99.7	345	23	US-09-823-033-2	Sequence 2, Appli
39	1728	99.7	345	23	US-09-852-209-3	Sequence 3, Appli
40	1728	99.7	345	23	US-09-852-209A-3	Sequence 3, Appli
41	1728	99.7	345	24	US-09-918-585A-488	Sequence 488, App
42	1728	99.7	345	24	US-09-923-995-4	Sequence 4, Appli
43	1728	99.7	345	24	US-09-929-404-2	Sequence 2, Appli
44	1728	99.7	345	25	US-09-978-187B-488	Sequence 488, App
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ALIGNMENTS

RESULT 1  
PCT-US99-22668-5  
; Sequence 5, Application PC/TUS9922668B  
; GENERAL INFORMATION:  
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; FILE OF INVENTION: THEREFOR, AND USES THEREOF  
; TITLE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER  
; CURRENT APPLICATION NUMBER: PCT/US99/22668B  
; CURRENT FILING DATE: 1999-09-30  
; EARLIER APPLICATION NUMBER: 60/102,461  
; EARLIER FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/108,109  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 60/110,749  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 60/113,002  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 60/135,426  
; EARLIER FILING DATE: 1999-05-21  
; EARLIER APPLICATION NUMBER: 60/144,022  
; NUMBER OF SEQ ID NOS: 39

DNA CODING

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-22668-5

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Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120

Qy 121 EYFPSEPGFCIHYNIVMPQTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180
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Qy 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKSITDV 300
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKSITDV 300

Qy 301 ALEHHEECDCVCRGSTGG 318
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RESULT 2
US-09-410-349A-5
; Sequence 5, Application US/09410349A
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Karl
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-349A-5

Query Match      100.0%; Score 1734; DB 18; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 ALEHHEECDCVCRGSTGG 318
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RESULT 3
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; Sequence 5, Application US/09852209
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Karl
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-209-5

Query Match      100.0%; Score 1734; DB 23; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
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Db 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
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QY 301 ALEHHEECDCVCRGSGTG 318
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; Sequence 5, Application US/09852209A
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-209A-5
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Query Match 100.0%; Score 1734; DB 23; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
Db 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
QY 121 EYPPSPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLNNNAITAFSTLEDLIRYLEPER 180
Db 121 EYPPSPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLNNNAITAFSTLEDLIRYLEPER 180
QY 181 WQDLDEDLVRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240
Db 181 WQDLDEDLVRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240
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Db 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300
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Db 301 ALEHHEECDCVCRGSGTG 318
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## RESULT 5

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; Sequence 5, Application US/10131600
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-5
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Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
Db 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
QY 121 EYPPSPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLNNNAITAFSTLEDLIRYLEPER 180
Db 121 EYPPSPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLNNNAITAFSTLEDLIRYLEPER 180
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Db 181 WQDLDEDLVRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240
QY 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300
Db 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300
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Db 301 ALEHHECDCVCRGSTGG 318

RESULT 6
US-10-303-997B-5
; Sequence 5, Application US/10303997B
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-303-997B-5

Query Match 100.0%; Score 1734; DB 29; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVIQ 60
Db 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVIQ 60
QY 61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRIRFVSD 120
Db 61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRIRFVSD 120
QY 121 EYFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180
Db 121 EYFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180
QY 181 WQDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVIREELKRTD 240
Db 181 WQDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVIREELKRTD 240
QY 241 TIFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDV 300
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDV 300
QY 301 ALEHHECDCVCRGSTGG 318
Db 301 ALEHHECDCVCRGSTGG 318

RESULT 7
PCT-US99-31025-29
; Sequence 29, Application PC/TUS9931025
; GENERAL INFORMATION:
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; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-29
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Query Match 99.7%; Score 1728; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVIQ 61
Db 7 KQFSSNKEQGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVIQ 66
QY 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRIRFVSD 121
Db 67 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRIRFVSD 126
QY 122 YFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 181
Db 127 YFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 186
QY 182 QLDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVIREELKRTD 241
Db 187 QLDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVIREELKRTD 246
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDVA 301
Db 247 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDVA 306
QY 302 LEHHECDCVCRGSTGG 318
Db 307 LEHHECDCVCRGSTGG 323
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RESULT 8
US-09-471-179-29
; Sequence 29, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471,179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-179-29
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Query Match 99.7%; Score 1728; DB 18; Length 323;
Best Local Similarity 100.0%; Pred. No. 8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVIQ 61
Db 7 KQFSSNKEQGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVIQ 66
QY 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKNQIRIRFVSD 121
```

Db 67 TFDERFGLPEDDICKYDFVEVEEPPSDGILGRWCGSGVPGKQISKGNQIRIRFVSDE 126  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 181  
Db 127 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 186  
QY 182 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVIREELKRTDT 241  
Db 187 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVIREELKRTDT 246  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVQLRPTKGVGLHKSLLTDVA 301  
Db 247 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVQLRPTKGVGLHKSLLTDVA 306  
QY 302 LEHHECDCVCRGSTGG 318  
Db 307 LEHHECDCVCRGSTGG 323

RESULT 9  
PCT-US01-43523-286  
; Sequence 286, Application PC/TUS0143523  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C331  
; CURRENT APPLICATION NUMBER: PCT/US01/43523  
; CURRENT FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 286  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
PCT-US01-43523-286

Query Match 99.7%; Score 1728; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 8.8e-165;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KFOFSSNKONGVQDPOHERIIITVSTNGSIHSRPFPHYPRNTTVLVRWVAEENVMQL 61  
Db 29 KFOFSSNKONGVQDPOHERIIITVSTNGSIHSRPFPHYPRNTTVLVRWVAEENVMQL 88  
QY 62 TFDERFGLPEDDICKYDFVEVEEPPSDGILGRWCGSGVPGKQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLPEDDICKYDFVEVEEPPSDGILGRWCGSGVPGKQISKGNQIRIRFVSDE 148  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVIREELKRTDT 241  
Db 209 QLDLEDLYRPTWOLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVIREELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVQLRPTKGVGLHKSLLTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVQLRPTKGVGLHKSLLTDVA 328  
QY 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345

RESULT 10  
PCT-US02-24563-286  
; Sequence 286, Application PC/TUS0224563  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C331  
; CURRENT APPLICATION NUMBER: PCT/US02/24563  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352







Search completed: November 25, 2003, 21:14:49  
Job time : 157.494 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:59 ; Search time 12.619 Seconds  
(without alignments)  
1293.384 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GKFQSSNKQNGVQDPQHE.....DVALEHHECDVCVRGSTGG 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 271250 seqs, 51324744 residues

Total number of hits satisfying chosen parameters: 271250

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1728	99.7	345	1	PCT-US03-26491-191
2	1728	99.7	345	5	US-09-457-066-2
3	1728	99.7	345	5	US-09-876-813-33
4	1728	99.7	345	6	US-10-648-593-191
5	1728	99.7	345	6	US-10-471-221-1
6	1728	99.7	345	7	US-60-487-610-1644
7	1728	99.7	345	7	US-60-485-450-1042
8	1720	99.2	345	5	US-09-830-320A-4
9	1559	89.9	345	5	US-09-457-066-43
10	1559	89.9	345	5	US-09-876-813-35
11	1325	76.4	302	5	US-09-876-813-54
12	1320.5	76.2	302	6	US-10-471-221-5
13	1266.5	73.0	303	5	US-09-876-813-57
14	1107	63.8	305	1	PCT-US00-28803-7
15	1098	63.3	316	5	US-09-876-813-55
16	1051.5	60.6	317	5	US-09-876-813-56
17	741	42.7	370	5	US-09-457-066-37
18	741	42.7	370	5	US-09-876-813-2
19	741	42.7	370	6	US-10-321-962-4
20	741	42.7	370	6	US-10-606-055-2
21	736	42.4	370	5	US-09-876-813-53
22	736	42.4	370	6	US-10-321-962-8
23	736	42.4	370	6	US-10-606-055-4
24	684	39.4	167	6	US-10-471-221-6
25	604	34.8	111	6	US-10-471-221-2
26	431	24.9	261	6	US-10-321-962-10

27	328.5	18.9	132	6	US-10-321-962-6	Sequence 6, Appli
28	320.5	18.5	154	6	US-10-321-962-12	Sequence 12, Appli
29	187	10.8	726	7	US-60-495-114-2251	Sequence 2251, Ap
30	181.5	10.5	730	5	US-09-830-320A-12	Sequence 12, Appli
31	181.5	10.5	730	7	US-60-495-114-2257	Sequence 2257, Ap
32	181.5	10.5	730	7	US-60-495-114-2260	Sequence 2260, Ap
33	181.5	10.5	730	7	US-60-495-114-2268	Sequence 2268, Ap
34	174	10.0	110	6	US-10-321-962-14	Sequence 14, Appli
35	173	10.0	823	7	US-60-495-114-2259	Sequence 2259, Ap
36	173	10.0	823	7	US-60-495-114-2266	Sequence 2266, Ap
37	173	10.0	823	7	US-60-495-114-2267	Sequence 2267, Ap
38	171	9.9	1015	7	US-60-495-114-1841	Sequence 1841, Ap
39	169	9.7	466	7	US-60-495-114-2262	Sequence 2262, Ap
40	169	9.7	717	7	US-60-495-114-2252	Sequence 2252, Ap
41	169	9.7	717	7	US-60-495-114-2253	Sequence 2253, Ap
42	169	9.7	717	7	US-60-495-114-2263	Sequence 2263, Ap
43	169	9.7	986	6	US-10-474-794-242	Sequence 242, App
44	169	9.7	986	7	US-60-495-114-2254	Sequence 2254, Ap
45	169	9.7	986	7	US-60-495-114-2264	Sequence 2264, Ap

ALIGNMENTS

RESULT 1  
PCT-US03-26491-191  
; Sequence 191, Application PC/TUS0326491  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/26491  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 191  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-26491-191

Query Match		99.7%	Score 1728;	DB 1;	Length 345;
Best Local Similarity		100.0%	Pred. No. 2.8e-139;	Mismatches 0;	Gaps 0;
Matches 317;		Conservative 0;			
Qy	2	KFQSSNKQNGVQDPQHE	IIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVW	IQL	61
Db	29	KFQSSNKQNGVQDPQHE	IIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVW	IQL	88
Qy	62	TFDRFGLGEPDDICKYDFVEVEE	PSDGTILGWCSGTVPVKOISKGNQIRIRFV	SDE	121
Db	89	TFDRFGLGEPDDICKYDFVEVEE	PSDGTILGWCSGTVPVKOISKGNQIRIRFV	SDE	148
Qy	122	YFSEPFCHYINVMQFTEAVSP	SVLPSPSALPLDLNNAITAFSTLEDLIRYLEP	SRW	181
Db	149	YFSEPFCHYINVMQFTEAVSP	SVLPSPSALPLDLNNAITAFSTLEDLIRYLEP	SRW	208
Qy	182	QLDLEDYRPTWQLLGKAFVFG	RKSRVVDLNLITVEEVLVYSCTPRNFVSIR	EELKRTDT	241
Db	209	QLDLEDYRPTWQLLGKAFVFG	RKSRVVDLNLITVEEVLVYSCTPRNFVSIR	EELKRTDT	268
Qy	242	IFWPGCLLVKRCGNCACCLH	NCNCCVSKTKKHEVLOLRPKTVRGHLKSL	TDVA	301
Db	269	IFWPGCLLVKRCGNCACCLH	NCNCCVSKTKKHEVLOLRPKTVRGHLKSL	TDVA	328
Qy	302	LEHHECDVCVRGSTGG	318		
Db	329	LEHHECDVCVRGSTGG	345		

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RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match          99.7%; Score 1728; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88

Qy  62 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148

Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYCTPRNFSVSIREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYCTPRNFSVSIREELKRTDT 268

Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 328

Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 3
US-09-876-813-33
; Sequence 33, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57

Query Match          99.7%; Score 1728; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88

Qy  62 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148

Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYCTPRNFSVSIREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYCTPRNFSVSIREELKRTDT 268

Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 328

Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-813-33
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Query Match          99.7%; Score 1728; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88

Qy  62 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148

Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYCTPRNFSVSIREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYCTPRNFSVSIREELKRTDT 268

Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 328

Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345
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RESULT 4
US-10-648-593-191
; Sequence 191, Application US/10648593
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 191
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-191
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Query Match          99.7%; Score 1728; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88

Qy  62 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPESDGTTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148

Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
```

QY 182 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 241  
Db 209 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCRGSTGG 318  
Db 329 LEHHECDVCVCRGSTGG 345  
RESULT 5  
US-10-471-221-1  
; SEQUENCE 1, Application US/10471221  
; GENERAL INFORMATION:  
; APPLICANT: Janssen Pharmaceutica N.V.  
; TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation  
; FILE REFERENCE: JAB 1687  
; CURRENT APPLICATION NUMBER: US/10/471,221  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US 60/274901  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-471-221-1

Query Match 99.7%; Score 1728; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.8e-139;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQL 61  
Db 29 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQL 88  
QY 62 TDFERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNIIRFVSDE 121  
Db 89 TDFERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNIIRFVSDE 148  
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 241  
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 241  
Db 209 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCRGSTGG 318  
Db 329 LEHHECDVCVCRGSTGG 345

RESULT 6  
US-60-487-610-1644  
; SEQUENCE 1644, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17

; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1644  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-487-610-1644

Query Match 99.7%; Score 1728; DB 7; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.8e-139;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQL 61  
Db 29 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQL 88  
QY 62 TDFERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNIIRFVSDE 121  
Db 89 TDFERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNIIRFVSDE 148  
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 241  
Db 209 QLDLEDLYRPTWQLLGRKAFVGRKSRVVDLNLTLTEEVRLYSCPRNFSVSIRELKRDTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCRGSTGG 318  
Db 329 LEHHECDVCVCRGSTGG 345

RESULT 7  
US-60-485-450-1042  
; SEQUENCE 1042, Application US/60485450  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: CHANG, Sheng-Yung  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001470  
; CURRENT APPLICATION NUMBER: US/60/485,450  
; CURRENT FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 47859  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1042  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-485-450-1042

Query Match 99.7%; Score 1728; DB 7; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.8e-139;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQL 61  
Db 29 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQL 88  
QY 62 TDFERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNIIRFVSDE 121  
Db 89 TDFERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNIIRFVSDE 148  
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

Qy 182 QLDLEDLYRPTWQLLGFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QLDLEDLYRPTWQLLGFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 268

Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328

Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345

RESULT 8  
US-09-830-320A-4  
; Sequence 4, Application US/09830320A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: GUEGLER, Karl J.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: AU-YOUNG, Janice K.  
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES  
; FILE REFERENCE: PF-0627 USN  
; CURRENT APPLICATION NUMBER: US/09/830,320A  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: PCT/US99/25458  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: US 60/183,024  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: US 60/155,216  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/172,233  
; PRIOR FILING DATE: 1999-05-17  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No.: 4163378CD1

US-09-830-320A-4  
Query Match 99.2%; Score 1720; DB 5; Length 345;  
Best Local Similarity 99.7%; Pred. No. 1.3e-138;  
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 61  
Db 29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 88

Qy 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148

Qy 122 YFPSEPGFCHYNTVMPQFTEAVSPVLPSPALFDLLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNTVMPQFTEAVSPVLPSPALFDLLNNAITAFSTLEDLIRYLEPERW 208

Qy 182 QLDLEDLYRPTWQLLGFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QLDLEDLYRPTWQLLGFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 268

Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328

Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345

RESULT 9  
US-09-457-066-43  
; Sequence 43, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-457-066-43

Query Match 89.9%; Score 1559; DB 5; Length 345;  
Best Local Similarity 87.1%; Pred. No. 6.7e-125;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 61  
Db 29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 88

Qy 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148

Qy 122 YFPSEPGFCHYNTVMPQFTEAVSPVLPSPALFDLLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNTVMPQFTEAVSPVLPSPALFDLLNNAITAFSTLEDLIRYLEPERW 208

Qy 182 QLDLEDLYRPTWQLLGFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QLDLEDLYRPTWQLLGFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT 268

Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328

Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGNAGG 345

RESULT 10  
US-09-876-813-35  
; Sequence 35, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 98-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463

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/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 345
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-876-813-35

Query Match      89.9%; Score 1559; DB 5; Length 345;
Best Local Similarity 87.1%; Pred. No. 6.7e-125;
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFTPTVNTVLVRLVAEENWVMIQL 61
DB 29 KLOLSDEKQNGVQDPQHERIITVSTNGSIHSPRFTPTVNTVLVRLVAEENWVMIQL 88
QY 62 TDFERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121
DB 89 TDFERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNHIRIRFVSDE 148
QY 122 YPSPRGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLPERP 181
DB 149 YPSPRGFCIHYSIMPQVETTSVPSVLPSPSLDLNNAITAFSTLEDLIRYLPERP 208
QY 182 QLDLEDLYRPTWQLGKAFVGRKSRVVDNLITTEVRVLYSCYTPRNFVSIREELKRTDT 241
DB 209 QVDSLKYFTWQLGKAFVGRKSKVNVNLLKEEVKLYSCYTPRNFVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKTKYKHYEVLQRPKTVGRGLHSLTDVA 301
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPRKTKYKHYEVLQRPKTVGRGLHSLTDVA 328
QY 302 LEHHEECDCVCRGSTGG 318
DB 329 LEHHEECDCVCRGNAGG 345

RESULT 11
US-09-876-813-54
/ Sequence 54, Application US/09876813
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/876,813
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: US/09/564,595
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: US 09/304,216
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/164,463
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 54
/ LENGTH: 302
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: fusion polypeptide
US-09-876-813-54

Query Match      76.4%; Score 1325; DB 5; Length 302;
Best Local Similarity 82.8%; Pred. No. 4.5e-105;
Matches 246; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: US 60/180,169
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 345
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-876-813-35

Query Match      89.9%; Score 1559; DB 5; Length 345;
Best Local Similarity 87.1%; Pred. No. 6.7e-125;
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFTPTVNTVLVRLVAEENWVMIQL 61
DB 29 KLOLSDEKQNGVQDPQHERIITVSTNGSIHSPRFTPTVNTVLVRLVAEENWVMIQL 88
QY 62 TDFERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121
DB 89 TDFERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNHIRIRFVSDE 148
QY 122 YPSPRGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLPERP 181
DB 149 YPSPRGFCIHYSIMPQVETTSVPSVLPSPSLDLNNAITAFSTLEDLIRYLPERP 208
QY 182 QLDLEDLYRPTWQLGKAFVGRKSRVVDNLITTEVRVLYSCYTPRNFVSIREELKRTDT 241
DB 209 QVDSLKYFTWQLGKAFVGRKSKVNVNLLKEEVKLYSCYTPRNFVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKTKYKHYEVLQRPKTVGRGLHSLTDVA 301
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPRKTKYKHYEVLQRPKTVGRGLHSLTDVA 328
QY 302 LEHHEECDCVCRGSTGG 318
DB 329 LEHHEECDCVCRGNAGG 345

RESULT 12
US-10-471-221-5
/ Sequence 5, Application US/10471221
/ GENERAL INFORMATION:
/ APPLICANT: Janssen Pharmaceutica N.V.
/ TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
/ FILE REFERENCE: JAB 1687
/ CURRENT APPLICATION NUMBER: US/10/471,221
/ CURRENT FILING DATE: 2003-09-05
/ PRIOR APPLICATION NUMBER: US 60/274901
/ PRIOR FILING DATE: 2001-03-09
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 282
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-471-221-5

Query Match      76.2%; Score 1320.5; DB 6; Length 282;
Best Local Similarity 80.1%; Pred. No. 9.9e-105;
Matches 254; Conservative 0; Mismatches 0; Indels 63; Gaps 1;

QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFTPTVNTVLVRLVAEENWVMIQL 61
DB 29 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFTPTVNTVLVRLVAEENWVMIQL 88
QY 62 TDFERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121
DB 89 TDFERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148
QY 122 YPSPRGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLPERP 181
DB 149 YPSPRGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLPERP 208
QY 182 QLDLEDLYRPTWQLGKAFVGRKSRVVDNLITTEVRVLYSCYTPRNFVSIREELKRTDT 241
DB 209 QLDLEDLYRPTWQLGKAFVGRKSRVVDNLITTEVRVLYSCYTPRNFVSIREELKRTDT 243
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKTKYKHYEVLQRPKTVGRGLHSLTDVA 301
DB 244 -----EVLQRPKTVGRGLHSLTDVA 265
QY 302 LEHHEECDCVCRGSTGG 318
DB 266 LEHHEECDCVCRGSTGG 282

RESULT 13
US-09-876-813-57
/ Sequence 57, Application US/09876813
/ GENERAL INFORMATION:
```



```
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-05-03
; PRIOR FILING DATE: 1999-11-10
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-57

Query Match 73.0%; Score 1266.5; DB 5; Length 303;
Best Local Similarity 78.9%; Pred. No. 4.3e-100;
Matches 240; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 20 ERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLEDPEDDICKY 79
DB 2 DETIQKGVQSGVQSPFPNSYPRNLLTWRHS-QENTRIQLVFDNQFGLSEAEINDICRY 60
QY 80 DFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNIQIRFVSDYEPSPGFCIHYNIVM 137
DB 61 DFVEVEDISTSIIRGWCWGHEVPRIKSRNQIKITKSDDYFVAKFGKIYSL-L 119
QY 138 PQTEA---VSPSLPPSALPLDLNNAITAFSTLEDLIRLYSPERWQDLEDLYRPTWQ 194
DB 120 EDFQAAASVSPSLPPSALPLDLNNAITAFSTLEDLIRLYSPERWQDLEDLYRPTWQ 179
QY 195 LLGKAFVGRKSRVDNLITTEVRLYSCPTPRNFSVIREELKRTDTIFWPGCLLVKRCG 254
DB 180 LLGKAFVGRKSRVDNLITTEVRLYSCPTPRNFSVIREELKRTDTIFWPGCLLVKRCG 239
QY 255 GNCACCLHNCQCQVPSKVTKKYHEVLQRLPKTGVRLHKS LTDVALEHHECDVCVRG 314
DB 240 GNCACCLHNCQCQVPSKVTKKYHEVLQRLPKTGVRLHKS LTDVALEHHECDVCVRG 299
QY 315 STGG 318
DB 300 STGG 303

RESULT 14
PCT-US00-28803-7
; Sequence 7, Application PC/TUS0028803
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Donoho, Gregory
; APPLICANT: Nehls, Michael
; APPLICANT: Halbun, Erin
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0070-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/28803
; CURRENT FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-10-16
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1999-10-29
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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-28803-7

Query Match 63.8%; Score 1107; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KFQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 61
DB 29 KFQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 88
QY 62 TFDERRFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIQIRFVSDE 121
DB 89 TFDERRFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIQIRFVSDE 148
QY 122 YFPSEPGFCIHYNIVMPQFTTEAVSPSLPPSALPLDLNNAITAFSTLEDLIRLYPERW 181
DB 149 YFPSEPGFCIHYNIVMPQFTTEAVSPSLPPSALPLDLNNAITAFSTLEDLIRLYPERW 208
QY 182 QLDLEDLYRPTWQLLGAFFVGRKSR 207
DB 209 QLDLEDLYRPTWQLLGAFFVGRKSR 234

RESULT 15
US-09-876-813-55
; Sequence 55, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1999-05-03
; PRIOR FILING DATE: 1999-11-10
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-55

Query Match 63.3%; Score 1098; DB 5; Length 316;
Best Local Similarity 67.1%; Pred. No. 9.7e-86;
Matches 210; Conservative 26; Mismatches 55; Indels 22; Gaps 5;

QY 19 HERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLEDPEDDICK 78
DB 1 HERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLEDPEDDICK 60
QY 79 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIQIRFVSDYEPSPGFCIHYNIVMP 138
DB 61 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIQIRFVSDYEPSPGFCIHYNIVMP 120
QY 139 QFTEAV-----SPSLPPSALPLDLNNAITAFSTLEDLIRLYPERWQ 182
DB 121 QFTEATNWSVTSSISGVSINSPSVTDPT-LIADALDKKIABFDTVEDLLKFNPSWQ 179
```

QY	183	LDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREBLKRTDTI	242
Db	180	EDLENNVLDTPRYGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVV	237
QY	243	FWFGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKHEVLQLRP---KTGVRGLHKS LTD	299
Db	238	FFPRCLLVQRCGGNCGCGTVNWRSCNCGTKVTKYKHEVLQFEFGHIKRRGRKTMALVD	297
QY	300	VALEHHEECDCVC	312
Db	298	IQLDHERCDCIC	310

Search completed: November 25, 2003, 21:15:40  
Job time : 13.619 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34 ; Search time 13.5655 Seconds  
(without alignments)  
2254.373 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GRKFSSNKEQNGVQDPQHE.....DVALEHHECDVCVRGSG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742	42.8	370	2 JC7591	spinal cord-derive
2	736	42.4	370	2 JC7592	spinal cord-derive
3	181.5	10.5	730	1 BMH1	procollagen C-endo
4	179.5	10.4	927	1 JQ0948	A5 antigen precurs
5	176	10.1	707	2 JC2218	procollagen C-endo
6	173.5	10.0	3623	2 T09456	intrinsic factor-B
7	173	10.0	823	1 A58788	procollagen C-endo
8	169	9.7	986	1 B58788	procollagen C-endo
9	169	9.7	991	2 I49540	procollagen C-endo
10	168	9.7	3623	2 T08618	intrinsic factor-B
11	154	8.9	449	2 A55362	procollagen I C-pr
12	148.5	8.6	1057	1 A39288	dorsal-ventral pat
13	143.5	8.3	686	1 A59271	Ra-reactive factor
14	139.5	8.0	1070	2 T31069	tollloid-BMP-1 like
15	138.5	8.0	597	2 S71352	metalloproteinase
16	138	8.0	705	1 C1HURB	complement subcomp
17	137.5	7.9	699	1 I54763	Ra-reactive factor
18	137.5	7.9	1524	2 T30337	polypeptide - Afri
19	133	7.7	1594	2 T30549	hensin - rabbit
20	132	7.6	419	2 S69207	vascular endotheli
21	130.5	7.5	1464	2 S58984	development protei
22	128	7.4	402	2 JH0403	procollagen I C-pr
23	127.5	7.4	767	2 T30018	hypothetical prote
24	127.5	7.4	3871	2 T22812	hypothetical prote
25	125	7.2	198	2 J50735	platelet-derived g
26	123.5	7.1	277	2 A41735	hyaluronate-bindin
27	120.5	6.9	245	1 TVCT5S	platelet-derived g
28	120.5	6.9	275	2 JVC6506	tumor necrosis fac
29	118.5	6.8	276	2 A47290	TSG-6 homolog

30 116.5 6.7 579 2 JC7629 membrane-type friz  
31 114.5 6.6 148 2 D49530 16K vascular endot  
32 114.5 6.6 241 1 PFHUG2 platelet-derived g  
33 112.5 6.5 200 2 I51551 platelet-derived g  
34 112.5 6.5 215 2 S08220 platelet-derived g  
35 112.5 6.5 226 2 I51550 platelet-derived g  
36 111.5 6.4 319 2 I51569 UVS.2 protein - Af  
37 110.5 6.4 2403 2 A59386 sanko - human  
38 110 6.3 166 2 JN0248 platelet-derived g  
39 109 6.3 197 2 S25096 platelet-derived g  
40 108.5 6.3 226 1 TVMVSS PDGF-related trans  
41 108 6.2 196 2 A37359 platelet-derived g  
42 104.5 6.0 232 2 A41551 vascular endotheli  
43 104 6.0 196 2 B28964 platelet-derived g  
44 104 6.0 211 1 PFHUG1 platelet-derived g  
45 103 5.9 770 2 D89447 protein F57C12.1 [

#### ALIGNMENTS

##### RESULT 1

JC7591  
spinal cord-derived growth factor-B precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001  
C;Accession: JC7591  
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.  
Biochem. Biophys. Res. Commun. 280, 733-737, 2001  
A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-  
A;Reference number: JC7591; MUID:2102670; PMID:11162582  
A;Accession: JC7591  
A;Molecule type: DNA  
A;Residues: 1-370 <HAM>  
A;Cross-references: DDBJ:AB033832  
C;Genetics:  
A;Gene: scdGF-B  
F;1-17/Domain: secretory signal sequence #status predicted <SIG>  
F;18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>  
F;52-170/Region: CUB domain #status predicted  
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr  
F;294-308/Region: conserved motif #status predicted

Query Match 42.8%; Score 742; DB 2; Length 370;

Best Local Similarity 46.6%; Pred. No. 1.2e-56;

Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;

QY 10 EQNGVQD-PQHERIITVSTNGSIHSRPHPTVPRNTVLVWELVAEENVMVQLTDFRFG 68

Db 42 ESNHLDLYRDETQVKGNGYQSPFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFG 100

QY 69 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVFGKQISKGNQIRIRFVSDEYFPSE 126

Db 101 LBAENDICRYDFVEVEDISETSTIIRGRCWGHKEVPPRIKSRNTQIKITFKSDDYFAK 160

QY 127 PGCIHYNVMPQTEAV-----SPSVLPSPALPLDLINNAITAFS 167

Db 161 PGFIYYSL-LEDQPAASSETNWESVTSISGVSNSPSVTDTPT-LIADALDKKIAEFD 218

QY 168 TLEDILRYLPERWOLDLRYPTWOLGKAFVGRKSRVVDNLNLTTEEVRVLSCTPRN 227

Db 219 TVEDLLKYFPESWQEDLENWYLDTPYRGSY-HSRKSK-VDLDRLNDDAKRYSCTERN 276

QY 228 FSVSIREELKRTDTIFWPGCLLVKRCGGNACCLHNCNECQVPSKVKYKTHEVLQRP- 286

Db 277 YSVNIREELKLANVVFPRCLLVQRCGNCGCGTVNWSCTCSGKTKVKYHEVLQPFPG 336

QY 287 --KTGVFGLHKLTDVALEHHECDVC 312

Db 337 HIKRGRGAKTMALVDIQLDHERCDIC 364

##### RESULT 2

A; Cross-references: DDBJ:AB052170  
C; Genetics:  
A; Gene: scdggf-B  
F; 1-17/Domain: secretory signal sequence #status predicted <SIG>  
F; 18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>  
F; 53-170/Region: CUB domain #status predicted  
F; 272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor #status predicted  
F; 294-308/Region: conserved motif #status predicted

Query Match	10.5%;	Score	181.5;	DB	1;	Length	730;
Best Local Similarity	37.3%;	Pred. No.	1.3e-07;				
Matches	50;	Conservative	20;	Mismatches	47;	Indels	17;
Gaps							7;
Qy	28	NGSTHSRFRPHYTPRNTVLVWRLVA-VEENWVIQLTDFERFGLPEDDDICKYDFVEVE	86				
Db	599	NGSTSPGWPKYEPNNKICHLQVLVATGYRISLQDFDFETEG-----NDVCKYDFVEVRS	653				
Qy	87	--PDGRTILRCWCSGTVPGKQISKGNQIRIRFVSDSEYFPSPGFCIHNNVMPQSTEAV	144				
Db	654	GLTADSKLHGKFCGS-EKEPVITSYNNMRVEFKSDNTV-SKKGPKAHF-----PSEK-	704				
Qy	145	SPSVLPSPSALPLDL	158				
Db	705	RPALQPPRGRPHQL	718				

RESULT 4  
JQ0948  
A5 antigen precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: JH0456; JQ0948  
R: Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.  
Nucleon 7, 295-307, 1991  
A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology  
A:Reference number: JH0456; MUID:91337458; PMID:1908252

A:Accession: G06400  
A:Molecule type: mRNA  
A:Residues: 1-527 <TAX>  
A:Cross-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01260.1; PID:g222963  
A:Experimental source: tadpole, brain  
A:Note: This protein has motifs homologous to complement components C1r and C1s and to C3 superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal  
C:Keywords: duplication; glycoprotein; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-927/Product: A5 antigen #status predicted <A5A>  
F:27-138/Domain: C1r/C1s repeat homology <C1R1>  
F:147-262/Domain: C1r/C1s repeat homology <C1R2>  
F:274-424/Domain: discoidin I amino-terminal homology <DN1>  
F:430-584/Domain: discoidin I amino-terminal homology <DN2>  
F:646-812/Domain: MAM homology <MAM>  
F:861-883/Domain: transmembrane #status predicted <TMM>  
F:150-261:300:523:844:Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 179.5; DB 1; Length 927;  
Best Local Similarity 31.6%; Pred. No. 2.7e-07;

QY 23 IVTVNGSIHSRPRPHYYTNTVTLWRLVAVENWIQLTFDERFGLDEDEDICKYDFV 82  
::: : : : : : : : : : : : : : : : : :  
Db 31 IKITSPSYLTAGYSHPSPORCEWLIOAPEHYQRIMINFNPHFDLEDRE--CKDYIV 87  
::: : : : : : : : : : : : : : : : : :  
QY 83 EV--EPPSDGTTILGRWCSGTVPVKOISKGNQIRIRFSVDYEPPEPSEPGFCIHYNIVMP-- 138  
::: : : : : : : : : : : : : : : : : :  
Db 88 EVIDGNANGQLLKVCYCGK-IAPSLPVSTGTPSIFRFVSDETPTG-AGFSIRVEVFTGP 145  
::: : : : : : : : : : : : : : : : : :  
QY 139 ----QTEA--VSPSVLPSPALPLDLNNNAITASTLEDLIRYLEPERWQIDLE 186

Best Local Similarity 26.4%; Pred. No 4.8e-06;  
Matches 92; Conservative 39; Mismatches 135; Indels 83; Gaps 22;

QY 3 POFSSNKQNG-----VDPQHERIITVTSGSIHSIPRPHYPRTNVLVRLVAIVEN 56  
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
910 FVKSSSTENHGFMAKPSAEDLACGEILTEST-GTIQSPGHNVYPHGINCTWHL-VQPN 967

QY 57 VNIQLTDFRRFGLEDDEDICKDFVEVEPEPSDGTILGRWCSTGTPGKOISKGNQIR 116  
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
968 HLTHLMF-BTFHLFEHYN--CTNDYLEVDYDTSSETLSGRYCGK-SIPPSLTSSGSLMLV 1023

QY 117 FVSDEVPFPGPCFIHYNIV-----MPQTEAVSPSVLPSPSALPLDLLNNAITAFSTLE 170  
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
1024 FVTDSDLAYE-GLFINEALSATAFLQDYDDLGIPTSP-----NFPNN----- 1067

QY 171 DLIRYLEPERWQDLBELYR---PTWQLLGKAFVGFKSRVRVDNLNLT-EVR----- 219  
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
1068 -----YPNWN-----ECIVRAITVRTGQLIAVHTNFSLEEAIG-NYYTDFLEIRDGGYEK 1116

QY 220 -----LY--SCTPRNFVSIRELK-RDTPI-----FWPCLLVKKGCGNCACLH 262  
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
1117 SPLIGHFYGSNLPPFTIISHSNKLWLKPKSQIDTRSGFSAYWDGS--STGGCGN----LT 1170

QY 263 NQNECQCVPKVKTKYHE---VLQLRPKTGVRLHKSLTDVALRHPEC 308  
DB |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
1171 TSSGTTISPNPYMPTYHSSCYWLNKSSHG-SAFELEKFDFLSEHPNC 1218

RESULT 7  
A58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human  
N/Alternate names: bone morphogenic protein splice form BMP-1/His  
C/Species: Homo sapiens (man)  
C/Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999  
C/Accession: A32788; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; H.  
R/Wozney J.M.: Science 242, 1528-1534, 1988  
A>Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A32788; PMID:89072730; PMID:3201241  
A/Acclusion: A32788  
A/Molecule type: mRNA  
A/Residues: 1-702,'EXRPALOPPRGPHOLKFRVQKNRTPQ' <WOZ>  
A/Cross-references: GB:M22488; NID:g179499; PIDN:AA51833.1; PID:g179500  
R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.  
J. Biol. Chem. 269, 32572-32578, 1994  
A/Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enc  
A/Reference number: A58788; PMID:95096114; PMID:7798260  
A/Acclusion: A58788  
A/Molecule type: mRNA  
A/Residues: 703-823 <TAK>  
A/Cross-references: GB:F35278; NID:G619423; PIDN:AAC41703.1; PID:g619424  
C/Genetics:  
A/Gene: GDB:BMP1; BMP-1  
A/Cross-references: GDB:I25203; OMIM:112264  
A/Map position: 8p21-8p21  
C/Function:  
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty  
C/Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology;  
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;  
F/1-22/Domain: signal sequence #status predicted <SIG>  
F/23-82/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>  
F/130-321/Domain: astacin homology <AST>  
F/322-431/Domain: Clr/Cls repeat homology <CLR1>  
F/435-544/Domain: Clr/Cls repeat homology <CLR2>  
F/551-587/Domain: EGF homology <EGF>  
F/591-700/Domain: Clr/Cls repeat homology <CLR3>  
F/738-752/Region: histidine-rich  
F/91.142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/163-319,185,200,322,348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-  
F/213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted  
F/214/Active site: Glu #status predicted  
F/565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match		10.0%; Score 173; DB 1; Length 823;
Best Local Similarity		35.6%; Pred. No. 8.4e-07; Indels 26; Gaps 7;
Matches		52; Conservative 19; Mismatches 49; Indels 26; Gaps 7;
QY	28	NGSIHSRPPHYPRNTVLVRLVA-VEENVWVQLTDFDERFGLDEDDICKYDFVEVEE 86
Db	599	NGSIISPGWPKPEYPPNKNCIWQLVAPTQYRISLQDFPFTEG-----NDVKCYDFVEVRS 653
QY	87	--PSDGTILGRWCGSTVPGKISKGNQIRIRFVSDYFPPSPGFCIHNVMPQTEAV 144
Db	654	GLTADSKLHGKFCGS-EKPEVITSQYNNMRVBFKSDNTV-SKKGFRAHFSVLEGAGDRH 711
QY	145	S-----PSVL-----PPSAL 154
Db	712	SHLSGLELLCPHALVDTVPAPPSAL 737
RESULT 8		
B58788		
N;Alternate names: bone morphogenetic protein 1, tolloid-like splice form		
C;Species: Homo sapiens (man)		
C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999		
C;Accession: A37278; B58788		
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew		
Science 242, 1528-1534, 1998		
A;Title: Novel regulators of bone formation: molecular clones and activities.		
A;Reference number: A37278; MUID:89072730; PMID:3201241		
A;Accession: A37278		
A;Molecule type: mRNA		
A;Residues: 1-702, 'EKRPALOPRGPHOLKFRVOKRNTPO' <WOZ>		
A;Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500		
R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.		
J. Biol. Chem. 269, 32572-32578, 1994		
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encoded		
A;Reference number: A58788; MUID:95096114; PMID:7798260		
A;Accession: B58788		
A;Molecule type: mRNA		
A;Residues: 703-986 <TAK>		
A;Cross-references: GB:L35279; NID:G619860; PIDN:AAC41710.1; PID:G619861		
C;Genetics:		
A;Gene: BMP-1		
A;Cross-references: GDB:1125203; OMIM:112264		
A;Map position: 8p21-8p21		
C;Function:		
A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type		
C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; F		
C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl		
F;1-22/Domain: signal sequence #status predicted <SIG>		
F;23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted		
F;130-321/Domain: astacin homology <AST>		
F;122-431/Domain: C1r/C1s repeat homology <C1R1>		
F;435-544/Domain: C1r/C1s repeat homology <C1R2>		
F;551-587/Domain: EGF homology <EGI>		
F;591-700/Domain: C1r/C1s repeat homology <C1R3>		
F;707-742/Domain: EGF homology <EG2>		
F;747-856/Domain: C1r/C1s repeat homology <C1R4>		
F;860-973/Domain: C1r/C1s repeat homology <C1R5>		
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted		
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66		
F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted		
F;214/Active site: Glu #status predicted		
F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted		
Query Match		9.7%; Score 169; DB 1; Length 986;
Best Local Similarity		39.4%; Pred. No. 2.3e-06;
Matches		43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;
QY	28	NGSIHSRPPHYPRNTVLVRLVA-VEENVWVQLTDFDERFGLDEDDICKYDFVEVEE 86
Db	599	NGSIISPGWPKPEYPPNKNCIWQLVAPTQYRISLQDFPFTEG-----NDVKCYDFVEVRS 653
QY	87	--PSDGTILGRWCGSTVPGKISKGNQIRIRFVSDYFPPSPGFCIHY 133

Query Match		10.0%; Score 173; DB 1; Length 823;
Best Local Similarity		35.6%; Pred. No. 8.4e-07; Indels 26; Gaps 7;
Matches		52; Conservative 19; Mismatches 49; Indels 26; Gaps 7;
Db	654	GLTADSKLHGKFCGS-EKPEVITSQYNNMRVBFKSDNTV-SKKGFRAHF 700
RESULT 9		
I49540		
C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;		
C;Species: Mus musculus (house mouse)		
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000		
C;Accession: I49540		
R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.		
Dev. Biol. 163, 175-183, 1994		
A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is r		
A;Reference number: I49540; MUID:94229342; PMID:8174772		
A;Accession: I49540		
A;Status: preliminary; translated from GB/EMBL/DBJ		
A;Molecule type: mRNA		
A;Residues: 1-991 <RES>		
A;Cross-references: GB:L24755; NID:G439606; PIDN:AAA37306.1; PID:G439607		
C;Genetics:		
A;Gene: Bmp-1		
C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;		
C;Keywords: hydrolase; metalloproteinase; zinc		
F;135-326/Domain: astacin homology <AST>		
F;556-592/Domain: EGF homology <EG1>		
F;596-705/Domain: C1r/C1s repeat homology <C1R>		
F;712-747/Domain: EGF homology <EG2>		
F;218,222,228,277/Binding site: zinc (His, His, Tyr) #status predicted		
F;219/Active site: Glu #status predicted		
Query Match		9.7%; Score 169; DB 2; Length 991;
Best Local Similarity		39.4%; Pred. No. 2.4e-06;
Matches		43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;
QY	28	NGSIHSRPPHYPRNTVLVRLVA-VEENVWVQLTDFDERFGLDEDDICKYDFVEVEE 86
Db	604	NGSITSGWPKPEYPPNKNCIWQLVAPTQYRISLQDFPFTEG-----NDVKCYDFVEVRS 658
QY	87	--PSDGTILGRWCGSTVPGKISKGNQIRIRFVSDYFPPSPGFCIHY 133
Db	659	GLTADSKLHGKFCGS-EKPEVITSQYNNMRVBFKSDNTV-SKKGFRAHF 705
RESULT 10		
T08618		
A;Description: intrinsic factor-B12 receptor CUBILIN precursor - rat		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002		
C;Accession: T08618		
R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayesen, J.H.; Rasmussen, H.H.; Brault,		
J. Biol. Chem. 273, 5235-5242, 1998		
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies		
A;Reference number: Z16459; MUID:98148073; PMID:9478979		
A;Accession: T08618		
A;Status: preliminary; translated from GB/EMBL/DBJ		
A;Molecule type: mRNA		
A;Residues: 1-3623 <MOE>		
A;Cross-references: EMBL:AF022247; NID:G3834379; PIDN:AAC71661.1; PID:G3834380		
C;Genetics:		
A;Gene: CUBILIN		
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology		
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membra		
F;1-20/Domain: signal sequence #status predicted <SIG>		
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>		
F;133-164/Domain: EGF homology <EGF1>		
F;436-467/Domain: EGF homology <EGF>		
Query Match		9.7%; Score 168; DB 2; Length 3623;
Best Local Similarity		25.8%; Pred. No. 1.4e-05;
Matches		88; Conservative 46; Mismatches 125; Indels 82; Gaps 22;
QY	4	QFSNKEQNGVQDQDHERIITVSTNGSIHSRPPHYPRNTVLVRLVAEENVWVQLTTF 63

Db 924 KFSDDKLECG-----EVLTAET-GIEBSPGHPNVYPRGVNCTHWV-VORGQLIRLF 974  
QY 64 DERFGLDEDDICKYDFVEVEPEPSDGTTLGRWCGSGTVPGRQISKGNQIRIRFVSDYF 123  
Db 975 SG-FYLEFHYN--CTNDYLEIYDAAQTFLGRYCGK-SIPPSLTNSNSIKLIFVSDSAL 1030  
QY 124 PSEPGGCIHY-----NIVMPOFTEAVSPVLV--PSALPLDL-----LNNAI--- 163  
Db 1031 AHE-GFSINVEALDASSVCLDYDTDFNGMLSPFNPNYPSNWEICIRYITVGLNQIALH 1089  
QY 164 -TAFSTLED-----LIRYLEPERWQDLDELVRPTWQLLQKAFVGRKSRVDNLNLTSE 217  
Db 1090 FTDF-TLEDYFGSQCVDFVE-----IRGGYETSPLVG---IY--CGSVLPPTIISHS 1136  
QY 218 VRLY-----SCTPNFVSIREELKRTDTTIFMPCGLLVKRCGNCACCLHNCQCQV 270  
Db 1137 NKLWLKFKSAAUTAGFSA-----YWDGS--STGCGN-----LTPTGVLTS 1178  
QY 271 PSKVTYKHYE--VLOLRPKTGVGRGLHKSITDVALEHHEEC 308  
Db 1179 PNYPMYPYHSSECYWELEASHG-SPFELEFQDPHLEHHPSC 1218  
RESULT 11  
A55362  
procollagen I C-proteinase enhancer protein precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999  
C:Accession: A55362  
R:Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show  
J. Biol. Chem. 269, 26280-26285, 1994  
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, g  
A:Reference number: A55362; MUID:95014462; PMID:7523404  
A:Accession: A55362  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-449 <TA>  
A:Cross-references: GB:L33799; NID:g642907; PIDN:AAA61949.1; PID:g642908  
C:Genetics:  
A:Gene: GDB:PCOLCE  
A:Cross-references: GDB:305468; OMIM:600270  
A:Map position: 7q21.3-q22  
C:Superfamily: C1r/C1s repeat homology  
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-449/Product: #status predicted <MAT>  
F:37-146/Domain: C1r/C1s repeat homology <C1R1>  
F:159-270/Domain: C1r/C1s repeat homology <C1R2>  
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 8.9%; Score 154; DB 2; Length 449;  
Best Local Similarity 33.8%; Pred. No. 1.8e-05;  
Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;  
QY 29 GSITHSPRPHT-YPRNTVLVRLVAVENWVQLTDFRFGLEDPEDDICKYDFVEY--- 84  
Db 168 GTLTTPNWPESDYPGIGCSWHIAPPDQV-IALT-F-EKFDLE--PDTYCKRYSVSFNG 223  
QY 85 EEFSDGTILGRWCGSGTVPGRQISKGNQIRIRFVSDYFSEPGFCIHYNVMPQFT--- 141  
Db 224 AVSDDSRRLGKFCGD-AVPGISSEGNNLLVQFVSDLSVTAD-GFSASYK-TLPRGTAK 280  
QY 142 -----EAVSPSV-LPPSALP 155  
Db 281 GQGPGPKRGTEPKYKLPKSP 302  
RESULT 12  
A39288  
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanoga  
C:Species: Drosophila melanogaster  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A39288  
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.  
Cell 67, 469-481, 1991  
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone  
A:Reference number: A39288; MUID:92034970; PMID:1840509  
A:Accession: A39288  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1057 <SHI>  
A:Cross-references: GB:M76976; NID:gi57305; PIDN:AAA28491.1; PID:gi57306  
C:Genetics:  
A:Gene: FlyBase:tld  
A:Cross-references: FlyBase:FBgn0003719  
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s rei  
C:Keywords: duplication; hydrolase; metalloproteinase; zinc  
F:136-329/Domain: astacin homology <AST>  
F:352-464/Domain: C1r/C1s repeat homology <C1R1>  
F:468-578/Domain: C1r/C1s repeat homology <C1R2>  
F:585-620/Domain: EGF homology <EG1>  
F:624-740/Domain: C1r/C1s repeat homology <C1R3>  
F:747-896/Domain: EGF homology <EG2>  
F:787-896/Domain: C1r/C1s repeat homology <C1R4>  
F:900-1013/Domain: C1r/C1s repeat homology <C1R5>  
F:221,225,231,280/Binding site: zinc (His, His, Tyr) #status predicted  
F:222/Active site: Glu #status predicted  
Query Match 8.6%; Score 148.5; DB 1; Length 1057;  
Best Local Similarity 38.0%; Pred. No. 0.00015;  
Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;  
QY 23 ITVSTNGSIHSPRPHTYPRNTVLVRLVAVENWVQLTDFRFGLEDPEDDICKYDFV 82  
Db 472 LKLTQKSIDSPNYPMDYMDKCVWRITA-PDNHQVALKF-QSFELE--KHDCGAYDFV 527  
QY 83 EVEE--PSDGTILGRWCGSGTVPGRQISKGNQIRIRFVSD 120  
Db 528 EIRKGNHSDSRLIGRCGDKLPNPK-TRSNQWIRFVSD 566  
RESULT 13  
A59271  
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human  
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)  
C:Species: Homo sapiens (man)  
C>Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
C:Accession: A59271  
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaesble, W.J.; Laursen, S.B.; Poulsen, I  
Nature 386, 506-510, 1997  
A:Title: A second serine protease associated with mannan-binding lectin that activates  
A:Reference number: A59271; MUID:97242412; PMID:9087411  
A:Accession: A59271  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-686 <JEN>  
A:Cross-references: GB:T09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627  
A:Experimental source: tissue liver  
A:Note: submitted to GenBank, December 1996  
A:Note: parts of this sequence, including the amino end of the mature protein, were det  
C:Genetics:  
A:Gene: GDB:MASP2  
A:Cross-references: GDB:6071500  
A:Map position: 1p36.2-1p36.3  
C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor  
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-444, 445-686/Product: Ra-reactive factor 2 #status predicted <MAT>  
F:13-134/Domain: C1r/C1s repeat homology <C1R1>  
F:142-180/Domain: EGF homology <EGF>  
F:184-293/Domain: C1r/C1s repeat homology <C1R2>  
F:300-361/Domain: complement factor H repeat homology <FH1>  
F:366-430/Domain: complement factor H repeat homology <FH2>  
F:445-679/Domain: trypsin homology <TRY>  
F:72-90, 142-156, 152-165, 167-180, 184-211, 241-259, 300-348, 328-361, 366-412, 396-430, 434-557

F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted  
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 8.3%; Score 143.5; DB 1; Length 686;  
Best Local Similarity 32.1%; Pred. No. 0.00025;  
Matches 34; Conservative 25; Mismatches 42; Indels 5; Gaps 4;

QY 28 NGSIIHSRPHPHYPRNTVLVWRLVAVENVVQLTFDERFGLDEPDDICKYDFVEVEEP 87  
DB 193 SGEISPEYPRYPKSSCTYS-ISLEGFVSILDFVSGFDVTHPETCLCYDFLKIQ-- 249  
QY 88 SDGTLGRWCGSGTVPGKQISKNQIRIRFVSDEYFSPGFCIH 133  
DB 250 TDEEHGPGCGK-TLPHRIETKSNVTIIFVDE-SGDHTGWLHY 293

RESULT 14  
T31069  
tolloid-BMP-1 like protein 1 - California sea hare  
N/Alternate names: Probable metalloprotease TBL-1  
C/Species: Aplysia californica (California sea hare)  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 18-Aug-2000  
C/Accession: T31069  
R/Liu, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Byrne, J.H.; B  
J. Neurosci. 17, 755-764, 1997  
A/Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme  
A/Reference number: Z29965; MUID:98007484; PMID:8987797  
A/Accession: T31069  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1070 <LIU>  
A/Cross-references: EMBL:U57369; NID:G1899041; PID:G1899042; PIDN:AAC47485.1  
C/Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s rep

Query Match 8.0%; Score 139.5; DB 2; Length 1070;  
Best Local Similarity 21.9%; Pred. No. 0.00095;  
Matches 70; Conservative 36; Mismatches 102; Indels 111; Gaps 17;

QY 29 GSITHSRPHYPRNTVLVWRLVAVENVVQL--TFDERFGLDEPDDICKYDFVEVE 85  
DB 529 GFLNSPAYDEYSGDKVCEW-VITVREGYQVAFETAFTEF---DPD---CAYDYVIR 581  
QY 86 --RPSDGTILGRWCGSGTVPGKQISKNQIRIRFVSDEYFSPGFCIH-- 133  
DB 582 DGTKDSPLVGTTCGRFT-PPNALSTRHLVYKVSDESM-QKGGSASYLEVDECEGE 639  
QY 134 -----NIVMPQFTEAVSPSV 148  
DB 640 DHGCEHVCVNTLGSYECTKIGYELHSDGKKCKACGGYLDAPSGTISPSF-----PDL 694  
QY 149 LPSPALPLDLLNNAITAFS-----TLEDLIRYLEPERWQLDLBLYRPTWQLLGAFFVG 203  
DB 695 YFPD-----KNCVWHISAPKGHILTIVNTHMDLE-WRGECEL-----DFRVVTVVG 741  
QY 204 RKSRRVDNLITBEVRLYSTCPNFSVS--IRBELKRTDTIFWPGCLL-----VKRCGGN 256  
DB 742 NKER-----LQGYCGFMAPPISITLSNELRIEFSDDTLQKTGFSMDYADVDECASS 795  
QY 257 CACCLHNCN-----ECQC 269  
DB 796 NGGCKHICENTVGSFHCSC 814

RESULT 15  
S71352  
metalloproteinase (EC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracentrotus livid  
N/Alternate names: Gene tolloid protein homolog  
C/Species: Paracentrotus lividus (common urchin)  
C/Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 17-Mar-1999  
C/Accession: S71352; A44880; S22060  
R/thomond, G.; Ghiglione, C.; Lepage, T.; Gache, C.  
Eur. J. Biochem. 238, 744-751, 1996

A/Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a  
A/Reference number: S71352; MUID:96300240; PMID:8706676  
A/Accession: S71352  
A/Molecule type: DNA  
A/Residues: 1-597 <LHO>  
A/Cross-references: EMBL:X65721; NID:e956534; PID:e46942  
A/Experimental source: sperm  
A/Note: the authors translated the codon GCT for residue 11 as Val, AAC for residue 57;  
R/Lepage, T.; Ghiglione, C.; Gache, C.  
Development 114, 147-163, 1992  
A/Title: Spatial and temporal expression pattern during sea urchin embryogenesis of a  
ral patterning gene tolloid.  
A/Reference number: A44880; MUID:92249197; PMID:1339338  
A/Accession: A44880  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-7, 'S', '9-10, 'V', '12-28, 'H', '30-72, 'D', '74-77, 'SK', '80-81, 'I', '83-232, 'R', '234-2;  
9-571, 'N', '573-584, 'D', '586-595, 'D', '597 <LEP>  
A/Cross-references: EMBL:X56224; NID:G10928; PID:G10929  
A/Experimental source: embryo  
A/Note: sequence extracted from NCBI backbone (NCBIP:99979)  
C/Genetics:

A/Gene: BP10  
A/Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2  
C/Superfamily: C1r/C1s repeat homology; astacin homology  
C/Keywords: hydrolase; metalloproteinase; zinc  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-597/Product: metalloproteinase 10, blastula #status predicted <MAT>  
F:102-295/Domain: astacin homology <AST>  
F:339-446/Domain: C1r/C1s repeat homology <CLR1>  
F:484-592/Domain: C1r/C1s repeat homology <CLR2>  
F:190,194,200/Binding site: zinc (His) #status predicted  
F:191/Active site: Glu #status predicted

Query Match 8.0%; Score 138.5; DB 2; Length 597;  
Best Local Similarity 24.4%; Pred. No. 0.00036;  
Matches 59; Conservative 44; Mismatches 92; Indels 47; Gaps 13;

QY 29 GSITHSRPHYPRNTVLVWRLVAVENVVQLTFDERFGLDEPDDICKYDFVEVEEP- 87  
DB 348 GVITSNPGRYDDNNACVYQIEGPGST-IELTFTE---MNIENHACRYDAVEIRKDD 403  
QY 88 --SDGTILGRWCGSGTVPGKQISKNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVS 145  
DB 404 INSDGE--KFCGN-TLPAVQISSGNQMLVSTSDPSITGR-GFRATYRIVILTTQLPD 458  
QY 146 PSVLPPSALPLDLLNNAIT-----AFSTLEDLI---RYLEPERWQLDLEDLYRPT 192  
DB 459 TTTI-STTTVPVPTTQATTDVTVVSCGGRFGTQGRVATPNY--PNYNDNLECVVIE 515  
QY 193 WOLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPNFSVSIREELKRTDTIFWPGCLLVKR 252  
DB 516 VEV-----GRVELDFDFVLEDET--NCRWDSLSINLGDGK-----IDMKM 556  
QY 253 CG 254  
DB 557 CG 558

Search completed: November 25, 2003, 21:05:29  
Job time : 13.5655 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:48 ; Search time 7.8869 Seconds  
(without alignments)  
1896.117 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GKQFSSNKQNGVDPQHE.....DVALEHHECDVCVCRGSTG 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	179.5	10.4	928	1 NRP1_XENLA	P28824 xenopus lae
2	176	10.1	707	1 BNP1_XENLA	P98070 xenopus lae
3	173.5	10.0	616	1 SPAN_STRPU	P98068 strongyloce
4	169	9.7	986	1 NRP1_HUMAN	P13497 homo sapien
5	169	9.7	991	1 BNP1_MOUSE	P98063 mus musculus
6	163.5	9.4	922	1 NRP1_RAT	Q9GWJ9 rattus norv
7	163.5	9.4	931	1 NRP2_HUMAN	O60462 homo sapien
8	163	9.4	925	1 NRP2_RAT	O35276 rattus norv
9	162.5	9.4	326	1 VEGD_RAT	O35251 rattus norv
10	160.5	9.3	923	1 NRP1_MOUSE	P97333 mus musculus
11	159.5	9.2	931	1 NRP2_MOUSE	O35375 mus musculus
12	159	9.2	1022	1 TLD_BRARE	O57460 brachydanio
13	158.5	9.1	923	1 NRP1_HUMAN	O14786 homo sapien
14	157	9.1	914	1 NRP1_CHICK	P79795 gallus gall
15	154	8.9	449	1 PCOL_HUMAN	Q15113 homo sapien
16	148.5	8.6	1057	1 TLD_DROME	P25723 drosophila
17	147	8.5	354	1 VEGD_HUMAN	O43915 homo sapien
18	143.5	8.3	686	1 MAS2_HUMAN	O00187 homo sapien
19	140	8.1	358	1 VEGD_MOUSE	P97946 mus musculus
20	139.5	8.0	597	1 BP10_PARLI	P43674 paracentrot
21	138.5	8.0	704	1 CRAR_MOUSE	P98064 mus musculus
22	138	8.0	639	1 BNP1_STRPU	P98066 strongyloce
23	138	8.0	705	1 CLR_HUMAN	P00736 homo sapien
24	137.5	7.9	699	1 CRAR_HUMAN	P48740 h complemen
25	132	7.6	419	1 VEGC_HUMAN	P49767 homo sapien
26	128	7.4	468	1 PCOL_MOUSE	O61398 mus musculus
27	128	7.4	468	1 PCOL_RAT	O08628 rattus norv
28	125	7.2	213	1 PDGA_RABIT	P34007 oryctolagus
29	125	7.2	415	1 VEGC_MOUSE	P97953 mus musculus
30	123.5	7.1	277	1 TSG6_HUMAN	P98066 homo sapien
31	120.5	6.9	245	1 PDGB_FELCA	P12919 felis silve
32	120.5	6.9	275	1 TSG6_MOUSE	O08859 mus musculus
33	118.5	6.8	276	1 TSG6_RABIT	P98065 oryctolagus

34	114.5	6.6	148	1 VEGH_ORFN7	P52585 orf virus (
35	114.5	6.6	241	1 PDGB_HUMAN	P01127 homo sapien
36	112.5	6.5	226	1 PDGA_XENLA	P13698 xenopus lae
37	111.5	6.4	514	1 UVS2_XENLA	P42664 xenopus lae
38	110	6.3	211	1 PDGA_MOUSE	P20033 mus musculus
39	109	6.3	204	1 PDGA_RAT	P28576 rattus norv
40	108.5	6.3	164	1 VEGA_CAPO	P28617 cavia porce
41	108.5	6.3	226	1 TSIS_SMSAV	P01128 simian sarc
42	105.5	6.1	207	1 VEGB_HUMAN	P49765 homo sapien
43	104.5	6.0	232	1 VEGA_HUMAN	P15692 homo sapien
44	104	6.0	211	1 PDGA_HUMAN	P04085 homo sapien
45	102.5	5.9	133	1 VEGH_ORFN2	P52584 orf virus (

## ALIGNMENTS

RESULT 1					
ID	NRP1_XENLA	STANDARD;	PRT;	928 AA.	
AC	P28824;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Neuropilin-1 precursor (AS protein) (AS antigen).				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBL_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=91337458; PubMed=1908252;				
RA	Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;				
RT	"The AS antigen, a candidate for the neuronal recognition molecule, has homologies to complement components and coagulation factors.";				
RL	Neuron 7:295-307(1991).				
CC	FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.				
CC	SUBCELLULAR LOCATION: Type I membrane protein.				
CC	TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER NEURONS.				
CC	SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.				
CC	SIMILARITY: Contains 2 CUB domains.				
CC	SIMILARITY: Contains 2 F5/8 type C domains.				
CC	SIMILARITY: Contains 1 MAM domain.				
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CC	EMBL; D10467; BAA01260.1; -.				
DR	HSSP; F12259; IC2T.				
DR	InterPro; IPR000859; CUB_domain.				
DR	InterPro; IPR000421; FA58_C.				
DR	InterPro; IPR000998; MAM_domain.				
DR	Pfam; PF00431; CUB; 2.				
DR	Pfam; PF00754; F5_F8_type_C; 2.				
DR	Pfam; PF00629; MAM; 1.				
DR	PRINTS; PR00020; MAMDOMAIN.				
DR	SMART; SM00042; CUB; 2.				
DR	SMART; SM00231; FA58C; 2.				
DR	SMART; SM00137; MAM; 1.				
DR	PROSITE; PS01180; CUB; 2.				

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DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00022; FA58C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 928
FT DOMAIN 22 860
FT TRANSMEM 861 883
FT DOMAIN 884 928
FT DOMAIN 27 141
FT DOMAIN 147 265
FT DOMAIN 275 424
FT DOMAIN 431 584
FT DOMAIN 646 812
FT DISULFID 27 54
FT DISULFID 82 104
FT DISULFID 147 173
FT DISULFID 206 228
FT DISULFID 275 424
FT DISULFID 431 584
FT CARBOHYD 150 151
FT CARBOHYD 261 261
FT CARBOHYD 300 300
FT CARBOHYD 523 523
FT CARBOHYD 844 844
SQ SEQUENCE 928 AA; 103416 MW; AF6B32380A4C789D CRC64;

Query Match 10.4%; Score 179.5; DB 1; Length 928;
Best Local Similarity 31.6%; Pred. No. 1.5e-07;
Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

Qy 23 ITVSTNGSIHSPRPHTYPRNTLVRLVAEENVMVLTDERPGLSDPDIDCKYDFV 82
Db 31 IKITSPSLTSGVPHSPPSQCEWLQAPEHYQRIINFNPHDPDLEDE---CKYDYV 87
Qy 83 EV--EPPSDGTLGRWCGSGTVPQKISQKQIRIRFVSDVEYFPGFCIHYNIVMP-- 138
Db 88 EVIDGNANGQLLGYCK--IAPSLVSTGSPISFIRVSDYETPG--AGFSTRYEVFKTP 145
Qy 139 ---QFTRA--VSPSLVPSALPLDLNNAITAFSTLEDLIRYLFERWQLDLE 186
Db 146 BCSRNFTSSNGVSKPKYKYPNALECTYIIFAPKMQEIV--LRFESFELEAD 197

RESULT 2
ID BMP1_XENLA STANDARD; PRT; 707 AA.
AC P98070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein 1 precursor (BC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94085787; PubMed=8262384;
RA Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT "Cloning and expression of cDNA encoding Xenopus laevis bone
RL morphogenetic protein-1 during early embryonic development.";
RL Gene 134:257-261(1993).
CC -!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
CC DIFFERENTIATION OF DEVELOPING ORGANS.
CC -!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 3 CUB domains.
-----
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EMBL; L12249; AAA16313.1; -.
PIR; JC2218; JC2218.
MEROPS; M12.005; -.
InterPro; IPR001506; Astacin.
InterPro; IPR000152; Asx_Hydroxyl.
InterPro; IPR000859; CUB_Domain.
InterPro; IPR001881; EGF_CA.
InterPro; IPR006209; EGF_Like.
InterPro; IPR006026; Nzn_Mtpeptidse.
InterPro; IPR006025; Zn_Mtpeptidse.
Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 3.
Pfam; PF00008; EGF; 1.
PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 3.
SMART; SM00179; EGF_CA; 1.
SMART; SM00235; ZnMG; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS01180; CUB; 3.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ?
FT PROPEP ? 83
FT CHAIN 84 707
FT DOMAIN 84 284
FT DOMAIN 285 397
FT DOMAIN 398 509
FT DOMAIN 510 551
FT DOMAIN 554 666
FT METAL 176 176
FT ACT_SITE 177 177
FT METAL 180 180
FT METAL 186 186
FT DISULFID 146 149
FT DISULFID 514 526
FT DISULFID 522 535
FT DISULFID 537 550
FT CARBOHYD 62 62
FT CARBOHYD 105 105
FT CARBOHYD 295 295
FT CARBOHYD 326 326
FT CARBOHYD 562 562
SQ SEQUENCE 707 AA; 80673 MW; 1B980D716DC3B8D CRC64;

Query Match 10.1%; Score 176; DB 1; Length 707;
Best Local Similarity 43.3%; Pred. No. 2.1e-07;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

Qy 28 NGSISPPPHPTYPNTVLVWELVAEENVMVLTDERPGLSDPDIDCKYDFVEVEE- 86
Db 562 NGSINSGPWPKYPPNKNICWQLVAPTQ--YRLSLFDDQ---FETEDNCKYDFVEVRSG 617
Qy 87 -PSDGTILGRWCGSGTVPQKISQKQIRIRFVSDVEYFPGFCIHYNIVMP- 129
Db 618 LTSDSLKHGKFCGS--ELPAVITSQYNNRIEFSNDTV--SKKGF 659

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RESULT 3  
 SPAN\_STRPU STANDARD; PRT; 616 AA.  
 AC P98068;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE SPAN protein precursor (EC 3.4.24.-).  
 GN SPAN.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92315921; PubMed=1618141;  
 RA Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C.;  
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of  
 RT sea urchin embryos, include one encoding a protein related to tollid  
 RT and BMP-1.";  
 RL Development 114:769-786(1992).  
 CC -1- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS  
 CC OF THE BLASTULA.  
 CC -1- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE  
 CC AND HATCHING).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC  
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 CC -----  
 CC EMBL; M84144; AAA30072.1; -;  
 CC HSSP; P28825; 1TAF.  
 CC MEROPS; M12.013; -;  
 CC InterPro; IPR001506; Astacin.  
 CC InterPro; IPR000859; CUB domain.  
 CC InterPro; IPR006210; EGF-like.  
 CC InterPro; IPR006210; IEGF.  
 CC InterPro; IPR006026; Zn Mpeptidse.  
 CC InterPro; IPR006025; Zn Mpeptidse.  
 CC Pfam; PF01400; Astacin; 1.  
 CC PRINTS; PR00480; ASTACIN.  
 CC SMART; SM00042; CUB; 2.  
 CC SMART; SM00181; EGF; 1.  
 CC SMART; SM00235; Zmcg; 1.  
 CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 CC PROSITE; PS01180; CUB; 2.  
 CC PROSITE; PS00022; EGF 1; 1.  
 CC PROSITE; PS01186; EGF 2; FALSE NEG.  
 CC Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;  
 CC Metalloprotease; EGF-like domain; Signal.  
 FT SIGNAL 1 16  
 FT PROPEP 17 93  
 FT CHAIN 94 616  
 FT DOMAIN 89 93  
 FT DOMAIN 94 295  
 FT DOMAIN 295 329  
 FT DOMAIN 340 450  
 FT DOMAIN 451 502  
 FT DOMAIN 503 614  
 FT METAL 190 190  
 FT ACT SITE 191 191  
 FT METAL 194 194  
 FT METAL 200 200  
 FT METAL

FT DISULFID 299 315 BY SIMILARITY.  
 FT DISULFID 305 317 BY SIMILARITY.  
 FT DISULFID 319 328 BY SIMILARITY.  
 SQ SEQUENCE 616 AA; 67902 MW; 397CD923FFB9B98 CRC64;  
 Query Match 10.0%; Score 173.5; DB 1; Length 616;  
 Best Local Similarity 27.0%; Pred. No. 2.9e-07;  
 Matches 70; Conservative 33; Mismatches 93; Indels 63; Gaps 14;  
 QY 29 GSISPRFPHTYPRNTVLVRLVAEENVMQLTFDERFGLDEDDICKYDFVEVEPS 88  
 Db 349 GEITSPNYPNVEDNTACVIEGPGST-IELTF---LDMEIETELCRYDAVEVRKDD 404  
 QY 89 DGTILGWCSGTVPGKQISKGNIIRFVSDVEYPPS--EPGCIHYNVMPQTFEAVSP 146  
 Db 405 INSIGKFCGN-TLPPVQISSNQMVSTSD---PSITRRGFKATYVIII-QTTTFST 459  
 QY 147 SVL---PPSALPLDLLNNAFAFSTLEDLYLRLPERWQLDLYRPTWLLGKAFVFG 203  
 Db 460 TTLQTPPSTTTTLQTPNPSTTLQT-----TNPSTTLQTTD--TPVIGCGTFV-G 509  
 QY 204 RKSRLVDNLNLTREVRVLYSCTPRNFVSIR-----BELKRTDTIF-----W 244  
 Db 510 VEGRVASPNY-----PNYDNLQCDYVIEVDGRRVELIFEDFGLDETTCRM 558  
 QY 245 PGCLL-----VKRG 254  
 Db 559 DSLMLNLNGIKVGMKMG 577  
 RESULT 4  
 BMP1 HUMAN  
 ID BMP1 HUMAN STANDARD; PRT; 986 AA.  
 AC P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 49, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)  
 DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).  
 GN BMP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).  
 RC TISSUE=Skin;  
 RX MEDLINE=96209868; PubMed=8643539;  
 RA Li S.W., Sieron A.L., Fertaia A., Hojima Y., Arnold W.V.,  
 RA Prockop D.J.;  
 RA "The C-proteinase that processes procollagens to fibrillar collagens  
 RT is identical to the protein previously identified as bone morphogenic  
 RT protein-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).  
 RX MEDLINE=89072730; PubMed=3201241;  
 RA Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,  
 RA Kriz R.W., Hewick R.M., Wang E.A.;  
 RA "Novel regulators of bone formation: molecular clones and  
 RT activities.";  
 RL Science 242:1528-1534(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).  
 RC TISSUE=Placenta;  
 RX MEDLINE=98160316; PubMed=9500680;  
 RA Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;  
 RT "Three alternatively spliced variants of the gene coding for the human  
 RT bone morphogenetic protein-1.";  
 RL J. Mol. Med. 76:141-146(1998).  
 RN [4]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).  
 RC TISSUE=Placenta;

Medline=95096114; PubMed=7798260;  
Takahara K., Lyons G.E., Greenspan D.S.;  
"Bone morphogenetic protein-1 and a mammalian tollid homologue (mtId)  
are encoded by alternatively spliced transcripts which are  
differentially expressed in some tissues.";  
J. Biol. Chem. 269:32572-32578 (1994).  
[5]  
DISULFIDE BOND IN METALLOPROTEINASE DOMAIN.  
MEDLINE=21336528; PubMed=11283002;  
Garrigue-Antar L., Barker C., Kadler K.E.;  
"Identification of amino acid residues in bone morphogenetic  
protein-1 important for procollagen C-proteinase activity.";  
J. Biol. Chem. 276:26237-26242 (2001).  
-!- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II  
AND II. INDUCES CARTILAGE AND BONE FORMATION.  
-!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at  
Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type  
III.  
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-  
ENDOPEPTIDASE ENHANCER PROTEIN.  
-!- ALTERNATIVE PRODUCTS.  
-!- Event=Alternative splicing; Named isoforms=7;  
Name=BMP1-3;  
IsoId=P13497-1; Sequence=Displayed;  
Name=BMP1-1;  
IsoId=P13497-2; Sequence=VSP\_005461, VSP\_005462;  
Name=BMP1-2; Sequence=Not described;  
IsoId=P13497-7; Sequence=Not described;  
Name=BMP1-4;  
IsoId=P13497-3; Sequence=VSP\_005463, VSP\_005464;  
Name=BMP1-5;  
IsoId=P13497-4; Sequence=VSP\_005465, VSP\_005466;  
Name=BMP1-6; Sequence=VSP\_005467, VSP\_005468;  
Name=BMP1-7;  
IsoId=P13497-6; Sequence=VSP\_005469, VSP\_005470;  
-!- TISSUE SPECIFICITY: Ubiquitous.  
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
-!- SIMILARITY: Contains 2 EGF-like domains.  
-!- SIMILARITY: Contains 5 CUB domains.  
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-----  
EMBL; U50330; AAA93462.1; -;  
EMBL; M22488; AAA51833.1; -;  
EMBL; Y08723; CAA69973.1; -;  
EMBL; Y08724; CAA69974.1; -;  
EMBL; Y08725; CAA69975.1; -;  
EMBL; L35278; AAC41703.1; -;  
EMBL; L35279; AAC41710.1; -;  
PIR; A37278; B59788.  
HSP; P00736; IAPQ.  
MEROPS; M12.005; -;  
Genew; HGNC:1067; BMP1.  
MTM; 112264; -;  
GO; GO:0005576; C:extracellular; NAS.  
GO; GO:0008237; F:metallopeptidase activity; NAS.  
GO; GO:0001502; P:cartilage condensation; TAS.  
GO; GO:0007275; P:development; TAS.  
InterPro; IPR001506; Astacin.  
InterPro; IPR000152; Asx hydroxyl.  
InterPro; IPR000859; CUB domain.  
InterPro; IPR001881; EGF\_Ca.  
InterPro; IPR006209; EGF\_like.  
InterPro; IPR006026; Zn Mtpeptidse.  
InterPro; IPR006025; Zn Mtpeptidse.



659 GLTADSKLHGKFGS-EKPEVITQNNRVEFKSDNTV-SKKGPKAHF 705

DB NRPI\_RAT STANDARD; PRT; 922 AA.  
AC Q9QWJ9;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).  
GN NRPI.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN SEQUENCE FROM N.A.  
RP STRAIN=Sprague-Dawley;  
RX MEDLINE=97433085; PubMed=9288754;  
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J., Ginty D.D.;  
RT "Neuropilin is a semaphorin III receptor.";  
CC [1]  
CC FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOREGULATION OF THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).  
CC SUBCELLULAR LOCATION: Type I membrane protein.  
CC TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.  
CC SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.  
CC SIMILARITY: Contains 2 CUB domains.  
CC SIMILARITY: Contains 2 F5/8 type C domains.  
CC SIMILARITY: Contains 1 MAM domain.

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-----  
EMBL; AF016296; AAC53337.1; -  
HGSP; P12259; 1CZT.  
InterPro; IPR000859; CUB domain.  
InterPro; IPR000421; FAS8 C.  
InterPro; IPR000998; MAM domain.  
Pfam; PF00431; CUB; 2.  
Pfam; PF00754; F5/F8 type\_C; 2.  
Pfam; PF00629; MAM; 1.  
PRINTS; PR00020; MAMDOMAIN.  
SMART; SM00042; CUB; 2.  
SMART; SM00231; FAS8C; 2.  
SMART; SM00137; MAM; 1.  
PROSITE; PS01180; CUB; 2.  
PROSITE; PS01285; FAS8C.1; 2.  
PROSITE; PS01286; FAS8C.2; 2.  
PROSITE; PS00022; FAS8C.3; 2.  
PROSITE; PS00740; MAM.1; 1.  
PROSITE; PS00060; MAM.2; 1.  
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 922 NEUROPILIN-1.  
FT DOMAIN 22 855 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 856 880 POTENTIAL.  
FT DOMAIN 881 922 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 141 CUB 1.  
FT DOMAIN 147 CUB 2.  
FT DOMAIN 275 F5/8 TYPE C 1.  
FT DOMAIN 431 F5/8 TYPE C 2.  
FT DOMAIN 645 MAM.  
FT DISULFID 27 54 PROBABLE.  
FT DISULFID 82 104 PROBABLE.  
FT DISULFID 147 173 PROBABLE.  
FT DISULFID 206 228 PROBABLE.  
FT DISULFID 275 424 BY SIMILARITY.  
FT DISULFID 431 583 BY SIMILARITY.  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD098B0F2E CRC64;

Query Match 9.4%; Score 163.5; DB 1; Length 922;  
Best Local Similarity 36.5%; Pred. No. 3.5e-06;  
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;  
QY 23 ITVSTNGSIHSPRPHTYPTNTVLVRLVAVENWVQLTFDERRGLEDDEDDICKYDFV 82  
DB 31 IKIENFGYLTSPGPHSHPEKCEWLIOAPEYQIRIMINFNHFDLEDKRD---CKYD 87  
QY 83 EV--EPPSDGTILRCWCGSGTVFGKQISKGNQIRIRFVSDEYFPPSEPGFCIHNYI 135  
DB 88 EVIDGENEGRLNGKFCGK-IAFSPVSSGPFIFKRVSD-YETHGAGFSIRVEI 140

RESULT 7  
NRPI\_HUMAN STANDARD; PRT; 931 AA.  
ID NRPI\_HUMAN STANDARD; PRT; 931 AA.  
AC OC0462; O14820; O14821;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).  
DE NRPI OR VEGF165R2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).  
RX MEDLINE=97470880; PubMed=9333348;  
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
RT "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III.";  
RT III.";  
RL Neuron 19:547-559 (1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM A22).  
RX TISSUE=Breast;  
RX MEDLINE=98188099; PubMed=9529250;  
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;  
RT "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";  
RL Cell 92:735-745 (1998).  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=20309748; PubMed=10748121;  
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;  
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";  
RL J. Biol. Chem. 275:18040-18045 (2000).  
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF. AND THE PLGF-2 ISOFORM OF PGF.  
CC -!- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH

CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Name=A22;

CC IsoId=060462-1; Sequence=Displayed;

CC Name=A0;

CC IsoId=060462-2; Sequence=VSP\_004342;

CC Name=A17;

CC IsoId=060462-3; Sequence=VSP\_004341;

CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -1- SIMILARITY: Contains 2 CUB domains.

CC -1- SIMILARITY: Contains 2 F5/8 type C domains.

CC -1- SIMILARITY: Contains 1 MAM domain.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; AF022859; AAC51788.1; -

CC EMBL; AF022860; AAC51789.1; -

CC EMBL; AF016098; AAC12922.1; -

CC HSPSP; P12259; 1CZT.

CC Genew; HGNC:8005; NRP2.

CC MIM; 602070; -

CC GO; GO:0005624; C:membrane fraction; TAS.

CC GO; GO:0004872; F:receptor activity; TAS.

CC GO; GO:0005021; F:vascular endothelial growth factor receptor. .; TAS.

CC GO; GO:0007411; P:axon guidance; TAS.

CC InterPro; IPR000859; CUB domain.

CC InterPro; IPR000421; FA58\_C.

CC Pfam; PF00431; CUB; 2.

CC Pfam; PF00754; F5 F8 type C; 2.

CC Pfam; PF00629; MAM; 1.

CC PRINTS; PR00020; MAMDOMAIN.

CC SMART; SM00042; CUB; 2.

CC SMART; SM00231; FA58C; 2.

CC SMART; SM00137; MAM; 1.

CC PROSITE; PS01180; CUB; 2.

CC PROSITE; PS01285; FA58C\_1; 2.

CC PROSITE; PS01286; FA58C\_2; 2.

CC PROSITE; PS50022; FA58C\_3; 2.

CC PROSITE; PS50060; MAM\_2; 1.

CC Transmembrane; Glycoprotein; Neuron; Signal; Repeat; Receptor;

CC Alternative splicing.

CC SIGNAL 1 20

CC CHAIN 21 931

CC DOMAIN 21 864

CC TRANSMEM 865 889

CC DOMAIN 890 931

CC DOMAIN 149 267

CC DOMAIN 277 427

CC DOMAIN 434 592

CC DOMAIN 642 802

CC DOMAIN 671 674

CC DISULFID 28 55

CC DISULFID 83 105

CC DISULFID 149 175

CC DISULFID 208 230

CC DISULFID 277 427

CC DISULFID 434 592

CC CARBOHYD 152 152

CC CARBOHYD 157 157

CC CARBOHYD 629 629

CC CARBOHYD 839 839

CC VARSPLIC 809 813

CC /FTID=VSP\_004341.

FT VARSPLIC 809 830 Missing (in isoform A0).

FT CONFLICT 602 602 /FTID=VSP\_004342.

FT SEQUENCE 931 AA; 104830 MW; 270CBAB69A0A797C CRC64;

Query Match 9.4%; Score 163.5; DB 1; Length 931;

Best Local Similarity 32.3%; Pred. No. 3.6e-06;

Matches 43; Conservative 19; Mismatches 64; Indels 7; Gaps 4;

Qy 5 FSSNKEQGVDPQHERIITVSTNGSIHSRPFPHYTPRNTVLVRLVAEENVMITLTFD 64

Db 14 YFSHQVRGQDPDPCGGRLNSKDAGYITSPGYPDYSHQNCCEWIVVAPENQKIVLNFN 73

Qy 65 ERFGLEDPEDDICKYDFEVE--EPSDGTILGRWCGSGTVEGKQISGNQIRIRFVSDEY 122

Db 74 PHFEIKHD--CKYDFEIRDGDSADLLGKCGN-IAPPTIISGSMLYIKFTSD-Y 128

Qy 123 FSPSPGFCIHNI 135

Db 129 ARQGAGFSLRYEI 141

RESULT 8

NRP2\_RAT STANDARD; PRT; 925 AA.

AC O35276;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165

DE receptor 2).

GN NRP2.

OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

ON NCBI\_TaxID=10116;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

EX MEDLINE=97433085; PubMed=9288754;

RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,

RA Ginty D.D.;

RT "Neuropilin is a semaphorin III receptor."

RL Cell 90:753-762(1997).

CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165

CC -1- AND VEGF-145 ISOFORMS OF VEGF. AND THE PLGF-2 ISOFORM OF PGF.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE

CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE

CC LINING IN THE RIBS.

CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -1- SIMILARITY: Contains 2 CUB domains.

CC -1- SIMILARITY: Contains 2 F5/8 type C domains.

CC -1- SIMILARITY: Contains 1 MAM domain.

CC -----

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CC -----

CC EMBL; AF016297; AAC53338.1; -

DR HSPSP; P12259; 1CZT.

DR InterPro; IPR000859; CUB domain.

DR InterPro; IPR000421; FA58\_C.

DR InterPro; IPR000998; MAM domain.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00754; F5 F8 type C; 2.

DR Pfam; PF00629; MAM; 1.

DR PRINTS; PR00020; MAMDOMAIN.

DR SMART; SM00042; CUB; 2.



## RESULT 10



```

NRP1_MOUSE
ID NR1_MOUSE STANDARD; PRT; 923 AA.
AC P97333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (A5 protein).
DN NR1 OR NR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BALB/c; TISSUE=Embryonic brain;
RX MEDLINE=96353149; PubMed=8748368;
RA Kawakami A., Kitsuawa T., Takagi S., Fujisawa H.;
RT "Developmentally regulated expression of a cell surface protein,
RL Neuropilin, in the mouse nervous system.";
RL J. Neurobiol. 29:1-17(1996).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM. IN ANGIOGENESIS. IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50086; BAA08789.1; -.
DR HSP; P12259; 1CZT.
DR MGP; MGI:106206; NRP.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5 F8 type C; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C 1; 2.
DR PROSITE; PS01286; FA58C 2; 2.
DR PROSITE; PS00022; FA58C 3; 2.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS00060; MAM 2; 1.
DR Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 923 NEUROPILIN-1.
FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 857 879 POTENTIAL.
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.

Query Match 9.3%; Score 160.5; DB 1; Length 923;
Best Local Similarity 36.5%; Pred. No. 6.4e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 923 AA; 103020 MW; 064B8A170796808 CRC64;

QY 23 ITVSTNGSIHSPRPHTYPTVTLVRLVAVENVWILQTFDERGLEDPEDDICKYDFV 82
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
31 IKIENPGYLTSPGYPHSYHPSEKCEWLIQAPEYQRIIINFNPHFDLEDRD---CKYQYV 87
QY 83 EV--EPPSDGTILGRCGSGTVPGKIQSKGNQIRIRFVSDYFPPSEPGFCIHNYI 135
Db || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
88 EVIDGENEGRLLWGKFCGK-IAPSPVSSGPFLLFKFVSD-YETHGAGFSIRYEI 140

RESULT 11
NRP2_MOUSE
ID NRP2_MOUSE STANDARD; PRT: 931 AA.
AC O35375; O35373; O35374; O35376; O35377; O35378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
DE NRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
RC STRAIN=BALB/c;
RX MEDLINE=97470888; PubMed=9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neuropilin-2, a novel member of the neuropilin family, is a high
RT affinity receptor for the semaphorins Sema 5 and Sema IV but not Sema
RT III.";
RL Neuron 19:547-559(1997).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -!- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=A22;
CC IsoId=O35375-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=O35375-2; Sequence=VSP_004344;
CC Name=A5;
CC IsoId=O35375-3; Sequence=VSP_004345;
CC Name=A17;
CC IsoId=O35375-4; Sequence=VSP_004343;
CC Name=B0;
CC IsoId=O35375-5; Sequence=VSP_004346;
CC Name=B5;
CC IsoId=O35375-6; Sequence=VSP_004347;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME
CC NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,
CC INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
CC -!- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS

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semaphorin family. Its expression has an averse effect on blood vessel number and integrity.

- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is secreted.

- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;

Name=1; Synonyms=Membrane-bound;

isoId=014786-1; Sequence=Displayed;

Name=2; Synonyms=Soluble, SNRP1;

isoId=014786-2; Sequence=VSP\_004339, VSP\_004340;

- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not seem to overlap. Isoform 1 is expressed by the blood vessels of different tissues. In the developing embryo it is found predominantly in the nervous system. In adult tissues, it is highly expressed in heart and placenta; moderately in lung, liver, skeletal muscle, kidney and pancreas; and low in adult brain. Isoform 2 is found in liver hepatocytes, kidney distal and proximal tubules.

- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.

- SIMILARITY: Contains 2 CUB domains.

- SIMILARITY: Contains 2 F5/8 type C domains.

- SIMILARITY: Contains 1 MAM domain.

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EMBL; AF018956; AAC51759.1; -

EMBL; AF016050; AAC12921.1; -

EMBL; AF145712; RAF44344.1; -

PDB; 1KEX; 28-JAN-03.

DR MIM; 602069; -

DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.

DR GO; GO:0007411; P:axon guidance; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR000859; CUB domain.

DR InterPro; IPR000421; FAS8 C.

DR InterPro; IPR000998; MAM\_domain.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00754; F5\_F8\_type\_C; 2.

DR PRINTS; PR00629; MAM; 1.

DR SMART; SM00042; CUB; 2.

DR SMART; SM00231; FAS8C; 2.

DR SMART; SM00137; MAM; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; FAS8C; 1; 2.

DR PROSITE; PS01286; FAS8C; 2; 2.

DR PROSITE; PS50022; FAS8C; 3; 2.

DR PROSITE; PS00740; MAM; 1; 1.

DR PROSITE; PS50060; MAM; 2; 1.

Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;

Receptor; Alternative splicing; 3D-structure.

CHAIN 1 21

FT CHAIN 22 923 NEUROFILIN-1.

FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 857 879 POTENTIAL.

FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 27 141 CUB 1.

FT DOMAIN 147 265 CUB 2.

FT DOMAIN 275 424 F5/8 TYPE C 1.

FT DOMAIN 431 583 F5/8 TYPE C 2.

FT DOMAIN 645 811 MAM.

FT DISULFID 27 54 PROBABLE.

FT

147 173 PROBABLE.

206 228 PROBABLE.

275 424 BY SIMILARITY.

431 583 BY SIMILARITY.

150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).

261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).

300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).

522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).

842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).

642 644 EFP -> GIK (in isoform 2).

FT VARSPLIC /FTid=VSP\_004339.

FT VARSPLIC Missing (in isoform 2).

FT VARSPLIC /FTid=VSP\_004340.

26 26 K -> E (IN REF. 1).

749 749 D -> H (IN REF. 2).

855 855 E -> D (IN REF. 2).

SEQUENCE 923 AA; ADEADC4A849B5D57 CRC64;

Query Match 9.1%; Score 158.5; DB 1; Length 923;

Best Local Similarity 35.7%; Pred. NO. 9.5e-06;

Matches 41; Conservative 18; Mismatches 49; Indels 7; Gaps 4;

QY 23 ITVTNGSIHSPRPHTYPRNTLVRLVAVENVYVWLTEDERFGLSDPEDDICKYDV 82

DB 31 IKIESPGVLTSPGYVHPSEKCEWLIQADPYQRIIMNFHFDLEDRD---CKIDYV 87

QY 83 EV--EPPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDVEYFPSEPGFCIHNI 135

DB 88 EVFDGENENGHRGKFCCK-TAPPPVSSGGFLFKFVSD-YETHGAGFSIRYEI 140

RESULT 14

NRPI\_CHICK

ID NRPI\_CHICK STANDARD; PRT; 914 AA.

AC P79795;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuropilin-1 precursor (A5 protein).

GN NRPI OR NRP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn; TISSUE=Embryonic brain;

RX MEDLINE=95324761; PubMed=7601310;

RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A., Fujisawa H.;

RT "Expression of a cell adhesion molecule, neuropilin, in the developing chick nervous system.";

RL Dev. Biol. 170:207-222(1995).

CC -! FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION PROPERTIES.

CC -! SUBCELLULAR LOCATION: Type I membrane protein.

CC -! TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM (LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G. BLOOD VESSELS IN THE ENTIRE EMBRYO.

CC -! SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.

CC -! SIMILARITY: Contains 2 CUB domains.

CC -! SIMILARITY: Contains 2 F5/8 type C domains.

CC -! SIMILARITY: Contains 1 MAM domain.

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CC -!- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE I  
CC PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.  
CC -!- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN  
CC METALLOPROTEINASE INHIBITORY ACTIVITY.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.  
CC -!- SIMILARITY: Contains 2 CUB domains.  
CC -!- SIMILARITY: Contains 1 NTR domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; L33799; AAA61949.1; ALT\_SEQ.  
CC EMBL; AB008549; BAA23281.1; -  
CC EMBL; AF053356; AAC78800.1; -  
CC EMBL; AF083655; AAD16041.1; -  
CC EMBL; BC000574; AAH00574.1; -  
CC EMBL; BC033205; AAH33205.1; -  
CC Genew; HGNC:8738; PCOLCE.  
CC MIM; 600270; -  
CC GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
CC GO; GO:0007275; P:development; TAS.  
CC InterPro; IPR000859; CUB domain.  
CC InterPro; IPR001134; Netrin\_C.  
CC Pfam; PF00431; CUB; 2.  
CC Pfam; PF01759; NTR; 1.  
CC SMART; SM00643; C345C; 1.  
CC SMART; SM00042; CUB; 2.  
CC PROSITE; PS01180; CUB; 2.  
CC Glycoprotein; Repeat; signal.  
KW POTENTIAL.  
FT SIGNAL 1 25  
FT CHAIN 26 449  
FT PROCOLLAGEN C-PROTEINASE ENHANCER  
FT PROTEIN.  
FT CUB 1.  
FT CUB 2.  
FT NTR.  
FT CLEAVAGE.  
FT SITE 287 288  
FT SITE 288 289  
FT SITE 293 294  
FT SITE 299 300  
FT SITE 303 304  
FT CLEAVAGE.  
FT SITE 29 29  
FT CARBOHYD N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 431 431 N-LINKED (GLCNAC...) (POTENTIAL).  
FT SEQUENCE 449 AA; 47972 MW; 3D88430158648796 CRC64;  
Query Match 8.9%; Score 154; DB 1; Length 449;  
Best Local Similarity 33.8%; Pred. No. 9.4e-06;  
Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;  
QY 29 GSITHSPFPHHT-YPRNTVLVRLVAVENWVIOITFDERFGLDEPDIDICKYDFVEY--- 84  
Db 168 GTITTFNWPESDPPGIGSCSWHIIAPPDQV-IALTFF-EKFDLE--PTYCRYDSVSFVNG 223  
QY 85 EEPESDGTILGRWCGSVTPGKQISKGNIQIRFVSDYFPEFSGFCIHNVIMPQFT--- 141  
Db 224 AVSDDSRLKFGCD-AVPGSISSEGNEILLVQFVSDLSVTAD-GFSASYK-TLPRGTAK 280  
QY 142 -----EAVSPSV-LPPSALP 155  
Db 281 GQGPGRKRGTEPKVLPKPSQP 302

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 25, 2003, 20:58:59 ; Search time 28.0774 Seconds  
(without alignments)  
2922.663 Million cell updates/sec

Title: US-09-852-209A-5  
Perfect score: 1734  
Sequence: 1 GKQFSNKQNGVDPQHE.....DVALEHHECDVCRCSTGG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23.3

- 1: sp archaea.\*
- 2: sp bacteria.\*
- 3: sp fungi.\*
- 4: sp human.\*
- 5: sp invertebrate.\*
- 6: sp mammal.\*
- 7: sp mbc.\*
- 8: sp organelle.\*
- 9: sp phase.\*
- 10: sp plant.\*
- 11: sp rodent.\*
- 12: sp virus.\*
- 13: sp vertebrate.\*
- 14: sp unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1728	99.7	345	4	Q9NRA1	Q9NRA1	homo sapien
2	1728	99.7	345	4	Q9UL22	Q9UL22	homo sapien
3	1559	89.9	345	11	Q9GY71	Q9GY71	mus musculus
4	1557	89.8	345	11	Q8C119	Q8C119	mus musculus
5	1541	88.9	345	11	Q9EQX6	Q9EQX6	rattus norv
6	1530	88.2	345	11	Q9JHV8	Q9JHV8	mus musculus
7	1524	87.9	345	13	Q9I946	Q9I946	gallus gall
8	1260	72.7	258	11	Q8K429	Q8K429	rattus norv
9	741	42.7	370	4	Q9GZP0	Q9GZP0	homo sapien
10	739.5	42.6	364	4	Q9BWV5	Q9BWV5	homo sapien
11	736	42.4	370	11	Q9EQT1	Q9EQT1	rattus norv
12	736	42.4	370	11	Q92517	Q92517	mus musculus
13	434	25.0	261	11	Q8K2L3	Q8K2L3	mus musculus
14	184.5	10.6	923	13	Q9QFX6	Q9QFX6	brachydanio
15	184.5	10.6	923	13	Q8AXP1	Q8AXP1	brachydanio
16	182	10.5	691	13	O57658	O57658	gallus gall

Q99JM4 mus musculus  
Q91925 xenopus lae  
O60494 homo sapien  
Q9WVM6 mus musculus  
O57381 xenopus lae  
Q9UQ00 homo sapien  
Q9Y6L7 homo sapien  
Q9Z135 rattus norv  
O70244 rattus norv  
Q9BPZ0 mus musculus  
Q8QZV7 mus musculus  
Q8H2E2 homo sapien  
Q9H2E4 homo sapien  
Q9H2D5 homo sapien  
Q9H2D4 homo sapien  
Q9H2E3 homo sapien  
Q9QX38 rattus norv  
O8J128 xenopus lae  
Q9CU53 canis famil  
Q9E190 homo sapien  
Q961H5 homo sapien  
Q9H2E1 homo sapien  
Q8UVR0 gallus gall  
Q8UVR9 gallus gall  
Q9DER7 gallus gall  
Q9UKZ9 homo sapien  
O57382 xenopus lae  
Q91ZE4 rattus norv  
Q9BRH3 homo sapien

ALIGNMENTS

RESULT 1

ID Q9NRA1 PRELIMINARY; PRT; 345 AA.  
AC Q9NRA1;  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)  
DE Platelet-derived growth factor C.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=20268201; PubMed=10806482;  
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,  
RA Backstrom G., Hellstrom M., Boström H., Li H., Soriano P.,  
RA Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;  
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-  
RT receptor.";  
RL Nat. Cell Biol. 2:302-309(2000).  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF244813; AAF80597.1; -;  
DR Genew; HGNC:8801; PDGFC  
DR InterPro; IPR000859; CUB\_domain.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS0278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 99.7%; Score 1728; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred.No. 1.4e-161; Indels 0; Gaps 0;  
Matches 317; Conservative 0; Mismatches 0;

QY 2 KFQSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVWQL 61  
 DB 29 KFQSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVWQL 88  
 QY 62 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121  
 DB 89 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 148  
 QY 122 YFPSEPGFCIHYNVMPQFTAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 DB 149 YFPSEPGFCIHYNVMPQFTAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
 QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSTPRNFSVSIREEKRTDT 241  
 DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSTPRNFSVSIREEKRTDT 268  
 QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTVGRGLHKS LTDVA 301  
 DB 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTVGRGLHKS LTDVA 328  
 QY 302 LEHHEECDCVCRGSGTG 318  
 DB 329 LEHHEECDCVCRGSGTG 345

RESULT 2  
 Q9UL22 PRELIMINARY; PRT; 345 AA.  
 AC Q9UL22;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
 DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).  
 GN HSCDGF OR PDGFC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Tsai Y.J., Lee R.K.K., Lin S.P.;  
 RT "Fallotein, a novel growth factor like gene identified in human uterus";  
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20317014; PubMed=10858496;  
 RA Hamada T., Ui-Tei K., Miyata Y.;  
 RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family";  
 RT FEBS Lett. 475:97-102(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21347863; PubMed=11297552;  
 RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;  
 RA "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That Binds to PDGF alpha and beta Receptor";  
 RT J. Biol. Chem. 276:27406-27414(2001).  
 RL J. Biol. Chem. 276:27406-27414(2001).  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR ENBL; AF091434; AAF00049.1; -;  
 DR ENBL; AB033831; BAB03266.1; -;  
 DR ENBL; AF260738; AAK51637.1; -;  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000072; PD\_growth\_factor.  
 DR Pfam; PF00431; CUB; 1  
 DR Pfam; PF00341; PDGF; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS50278; PDGF; 2; 1.  
 SQ SEQUENCE 345 AA; 39029 MW; CDE9B51F40633E78 CRC64;  
 Query Match 99.7%; Score 1728; DB 4; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-161;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KFQSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVWQL 61  
 DB 29 KFQSSNKEQNGVDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVWQL 88  
 QY 62 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121  
 DB 89 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 148  
 QY 122 YFPSEPGFCIHYNVMPQFTAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 DB 149 YFPSEPGFCIHYNVMPQFTAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
 QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSTPRNFSVSIREEKRTDT 241  
 DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSTPRNFSVSIREEKRTDT 268  
 QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTVGRGLHKS LTDVA 301  
 DB 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTVGRGLHKS LTDVA 328  
 QY 302 LEHHEECDCVCRGSGTG 318  
 DB 329 LEHHEECDCVCRGSGTG 345

RESULT 3  
 Q9QY71 PRELIMINARY; PRT; 345 AA.  
 ID Q9QY71;  
 AC Q9QY71;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
 DE Fallotein (Platelet-derived growth factor C).  
 GN PDGFC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;  
 RT "cDNA Cloning of fallotein from mouse ovary";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;  
 RA "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR ENBL; AF117608; AAF22516.1; -;  
 DR ENBL; AF266467; AAK58566.1; -;  
 DR ENBL; AK033734; BAC28455.1; -;



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DR EMBL; AK042767; BAC31358.1; -.
DR EMBL; AK052947; BAC35216.1; -.
DR MGD; MGI:1859631; PDGF; CUB; 1.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS0180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B04EA2 CRC64;

Query Match      89.9%; Score 1559; DB 11; Length 345;
Best Local Similarity 87.18; Pred. No. 6.1e-145;
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61
Db 29 KQLSSDKEQGVQDPQHERVVTISNGSIHSPKFPHTYPRNMVWRLVAEENVWQL 88

QY 62 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNHIRIRFVSDE 148

QY 122 YFPSEPGFCIHYNIMVQFTEAVSPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYSIIMPQVTTETSPSVLPSPSSLSLDDLNNAVTAFSTLEELIRYLEPDRW 208

QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCSTPRNFSVSIREELKRTDT 241
Db 209 QVLDLSLYKPTWQLLGKAFYLGKSKVNNLLKKEVKLYSCSTPRNFSVSIREELKRTDT 268

QY 242 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 328

QY 302 LEHHECDVCVRGSGTG 318
Db 329 LEHHECDVCVRGNAGG 345

Query Match      89.9%; Score 1559; DB 11; Length 345;
Best Local Similarity 87.18; Pred. No. 6.1e-145;
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61
Db 29 KQLSSDKEQGVQDPQHERVVTISNGSIHSPKFPHTYPRNMVWRLVAEENVWQL 88

QY 62 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNHIRIRFVSDE 148

QY 122 YFPSEPGFCIHYNIMVQFTEAVSPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYSIIMPQVTTETSPSVLPSPSSLSLDDLNNAVTAFSTLEELIRYLEPDRW 208

QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCSTPRNFSVSIREELKRTDT 241
Db 209 QVLDLSLYKPTWQLLGKAFYLGKSKVNNLLKKEVKLYSCSTPRNFSVSIREELKRTDT 268

QY 242 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 328

QY 302 LEHHECDVCVRGSGTG 318
Db 329 LEHHECDVCVRGNAGG 345

Query Match      89.8%; Score 1557; DB 11; Length 345;
Best Local Similarity 86.8%; Pred. No. 9.7e-145;
Matches 275; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61
Db 29 KQLSSDKEQGVQDPQHERVVTISNGSIHSPKFPHTYPRNMVWRLVAEENVWQL 88

QY 62 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNHIRIRFVSDE 148

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QY 122 YFPSEPGFCIHYNIMVQFTEAVSPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYSIIMPQVTTETSPSVLPSPSSLSLDDLNNAVTAFSTLEELIRYLEPDRW 208

QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCSTPRNFSVSIREELKRTDT 241
Db 209 QVLDLSLYKPTWQLLGKAFYLGKSKVNNLLKKEVKLYSCSTPRNFSVSIREELKRTDT 268

QY 242 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 328

QY 302 LEHHECDVCVRGSGTG 318
Db 329 LEHHECDVCVRGNAGG 345

RESULT 5
Q9EQX6 PRELIMINARY; PRT; 345 AA.
ID Q9EQX6
AC Q9EQX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Spinal cord-derived growth factor.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=1162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737 (2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033830; BAB19969.1; -.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS0180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match      88.9%; Score 1541; DB 11; Length 345;
Best Local Similarity 85.8%; Pred. No. 3.6e-143;
Matches 272; Conservative 28; Mismatches 17; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61
Db 29 KQLSSDKEQGVQDPQHERVVTISNGSIHSPKFPHTYPRNTVLVWRLVAEENVWQL 89

QY 62 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLDEDDICKYDFVEVEEPEPSDGTILGRWCGSGTVPGKQISKGNHIRIRFVSDE 148

QY 122 YFPSEPGFCIHYNIMVQFTEAVSPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYSIIMPQVTTETSPSVLPSPSSLSLDDLNNAVTAFSTLEELIRYLEPDRW 208

QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSCSTPRNFSVSIREELKRTDT 241
Db 209 QVLDLSLYKPTWQLLGKAFYLGKSKVNNLLKKEVKLYSCSTPRNFSVSIREELKRTDT 268

QY 242 IFWPGCLLVKRCGGNCACCLHNCNECCQVPSKVTKYKHYEVLQRLPKTGVRGLHKS LTDVA 301

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Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQVPRKVTYKXVHEVLQLRPKIGVGLHKS LTDVA 328
QY 302 LEHHECDCVCRGSTGG 318
Db 329 LEHHECDCVCRGNTEG 345

RESULT 6
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
organogenesis";
RL Mech. Dev. 96:209-213 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF286725; AAF91483.1; -
DR MGD; MGI:1859631; pdgfc.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 88.2%; Score 1530; DB 11; Length 345;
Best Local Similarity 85.8%; Pred. No. 4.4e-142;
Matches 272; Conservative 26; Mismatches 19; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMITQL 61
Db 29 KQSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMITQL 88
QY 62 TDFERFGLDEPDICKYDFVEVEEPPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSD 121
Db 89 TDFERFGLDEPDICKYDFVEVEEPPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSD 148
QY 122 YPSEPGCIHYNIMVQFTAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YPSEPGCIHYIIMPQVETTSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFVSIREELKRTDT 241
Db 209 QVLDLSLYKPTWQLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKXVHEVLQLRPKIGVGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKXVHEVLQLRPKIGVGLHKS LTDVA 328
QY 302 LEHHECDCVCRGSTGG 318
Db 329 LEHHECDCVCRGNAGG 345

RESULT 7
Q9I946 PRELIMINARY; PRT; 345 AA.
ID Q9I946
AC Q9I946;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Spinal cord-derived growth factor.
GN SCDGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Spinal cord;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BAB03265.1; -
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 87.9%; Score 1524; DB 13; Length 345;
Best Local Similarity 84.9%; Pred. No. 1.7e-141;
Matches 269; Conservative 28; Mismatches 20; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMITQL 61
Db 29 KFSFPGAKEQGVDPQHEKITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMITQL 88
QY 62 TDFERFGLDEPDICKYDFVEVEEPPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSD 121
Db 89 TDFERFGLDEPDICKYDFVEVEEPPSDGTILGRWCGSGSVPSRQISKGNQIRIRFVSD 148
QY 122 YPSEPGCIHYNIMVQFTAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YPSPQPGCIHYITLLVPHTEAPSPSLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKXVHEVLQLRPKIGVGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKXVHEVLQLRPKIGVGLHKS LTDVA 328
QY 302 LEHHECDCVCRGSTGG 318
Db 329 LEHHECDCVCKGNSEG 345

RESULT 8
Q8K429 PRELIMINARY; PRT; 258 AA.
ID Q8K429
AC Q8K429;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
RL Healing.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF08348; AAM47265.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
FT NON TER 1 258
FT SEQUENCE 258 AA; 29255 MW; 88625B98FCC3F8B CRC64;
SQ
Query Match 72.7%; Score 1260; DB 11; Length 258;
Best Local Similarity 85.6%; Pred. No. 1.1e-115;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
QY 15 QDPOHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVVIQLTDFRFGLEDPED 74
DB 1 QDPRHERVVTISGNSIHSPRPHTYPRNTVLVRLVAEENVRIQLTDFRFGLEDPED 60
QY 75 DICKYDFVEVEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYN 134
DB 61 DLCKYDFVEVEPEPSDGSVLGRWCGSGTVPGKTSKGNHIRFVSDYFPPSEPGFCIHY 120
QY 135 IVMQFTFAVSPULPPSALPIDLNNAITFSTLEDLIRVLEPERWQDLEDLVRPTWQ 194
DB 121 IIMQVTTETSPVLPSPSALDLNNAVTAFSTVEELIRLEPRWQIDLSLYKPTWP 180
QY 195 LLGKAFVGRKSRVVDLNLLEEVRLYSCTRNFVSVSIREELKRTDTTFWPCCLLVKCG 254
DB 181 LLGKAFVGRKSKAVNLLKEEVRLYSCTRNFVSVSIREELKRTDTTFWPCCLLVKCG 240
QY 255 GNCACCLHNCNECCQVP 271
DB 241 GNCACCLHNCNECCQVP 257
RESULT 9
Q9GZP0 PRELIMINARY; PRT; 370 AA.
ID Q9GZP0
AC Q9GZP0;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 23, Last sequence update)
DE SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth
DE factor long form) (Platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGFD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular Cloning of SCDFG-B, a Novel Growth Factor Homologous to
RT SCDFG/PDGF-C/fallotenein.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;

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RA Wistow G.;
RT "Iris-expressed Growth Factor (IEGF).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881;
RA Bergsten B., Eriksson U.;
RA Alitalo K., Ukkonen U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RP SEQUENCE FROM N.A.
RX MEDLINE=2123380; PubMed=11331882;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichtenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
CC -|- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033832; BAB18903.1; -.
DR EMBL; AF113216; AAG39287.1; -.
DR EMBL; AY027517; AAK20081.1; -.
DR EMBL; AF336376; AAK56136.1; -.
DR EMBL; AF335584; AAK38840.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
Query Match 42.7%; Score 741; DB 4; Length 370;
Best Local Similarity 46.6%; Pred. No. 2.2e-64;
Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;
QY 10 EONGVQD-PQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVVIQLTDFERG 68
DB 42 ESNHITDLYRRDETQVKGNGYVQSPFNLSLTLRLHS-QENTRIQLVFDNQFG 100
QY 69 LEDPDDICKYDFVEVEPEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSE 126
DB 101 LEEAENDICRVDFVEVEDEISESTIIRGWCGHKEVPPRIKSRTWQIKITFKSDDYFVAK 160
QY 127 PGFCIHYNIIVMPQFTEAV-----SPSVLPSPSALPIDLNNAITAFS 167
DB 161 PGFKIYSL-LSDFPQAAAASNTWESVTSSISGVSYNSPSVTDPT-LIADALDKIAED 218
QY 168 TLEDLIRVLEPERWQDLEDLVRPTWQLLGKAFVGRKSRVVDLNLLEEVRLYSCTRN 227
DB 219 TVEDLLKYFNPEWQEDLENMYLDFPRYGRSY-HDRKSK-VLDRLNDDAKRYSCTRN 276
QY 228 FSVSIREELKRTDTTFWPCCLLVKCGGNACCLHNCNECCQVPKSVTKKYHEVLQLRP- 286
DB 277 YSVNIREELKLANVFFPRCLLVQRCGCGGTWNRSCTNSGKTVKKYHEVLQFEPG 336
QY 287 --KTGVRGLHKSITDVALEHHEECDCVC 312
DB 337 HIKRGRKTAKTALVDIQLDHERCDDIC 364
RESULT 10
Q9BNV5 PRELIMINARY; PRT; 364 AA.
ID Q9BNV5
AC Q9BNV5;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)

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DE	Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).	
GN	IEGF.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxId=9606;	
GN	[1]	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=Iris;	
RC	Wistow G.;	
RT	"Iris-expressed Growth Factor (IEGF).";	
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testis;	
RA	Strausberg R.;	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY027518; AAK20082.1; -.	
DR	EMBL; BC030645; AAH30645.1; -.	
DR	InterPro; IPR000859; CUB domain.	
DR	InterPro; IPR000072; PD_growth_factor.	
DR	InterPro; IPR000531; TonB_boxC.	
DR	Pfam; PF00431; CUB; 1.	
DR	PROSITE; PS01180; CUB; 1.	
DR	PROSITE; PS02078; PDGF 2; 1.	
DR	PROSITE; PS00430; TONB_DEPENDENT_REC 1; 1.	
SQ	SEQUENCE 364 AA; 42166 MW; 245C53E8DDAE9EAC CRC64;	
Query Match 42.6%; Score 739.5; DB 4; Length 364;		
Best Local Similarity 47.0%; Pred. No. 3.1e-64;		
Matches 150; Conservative 51; Mismatches 89; Indels 29; Gaps 8		
Qy	18 QHERIITVSTGSIHSPRPHTYPTNTVLVRLVAEENVWVLTQTFDRFGLEDPEDDIC 77	
Db	45 RRDETQVKGNGYVQSPFPFNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLAEAEIDIC 103	
Qy	78 KYDFVEVEPSDGT--ILGRWCGSGTVPKGQISKGNQIRIRFVSDEYPPSEPGFCIHVNI 135	
Db	104 RYDFVEVEDISETSIIIRGWCGHEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSL 163	
Qy	136 VMQFTEAV-----SPSVLPSPALPLDLNNAITAFSTLEDLIRYL 176	
Db	164 -LEDFOPAASATNWESVTSSISGVSYNPSVTDPT-LIADALDKKIAEFDVEDULKYF 221	
Qy	177 EPERWQLDLEDLYRPTQWLLQKAFVGRKSRVVDLNLTLTEEVRLYSCTPRNFVSIREEL 236	
Db	222 NPESWQEDLNNYLDTPYRGESY-HDRKSK-VLDRLNDDAKRYSCTPRNVSVNIREEL 279	
Qy	237 KRTDTIFWPGCLLVKRCGNACCLHNCCEQCVSKVTKKHYEVLQLRP---KTGVRGL 293	
Db	280 KLANVVFPRCLLVQRCGNCCGTVNWRSCNTCSGKTVKKYHEVLQFEPFGHKKRGRAK 339	
Qy	294 HKSLTDVALEHHEGDCVC 312	
Db	340 TVALVDIQLDHHRCDCIC 358	
RESULT 11		
Q9EQT1	PRELIMINARY; PRT; 370 AA.	
AC	Q9EQT1	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	Spinal-cord derived growth factor-B.	
GN	RSCDGF-B.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX	NCBI_TaxId=10116;	
GN	[1]	
RP	SEQUENCE FROM N.A.	

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayaishizaki Y.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.,  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [8]  
RP SEQUENCE FROM N.A.  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF335583; AAA38839.1; -.  
DR EMBL; AK003359; BAB22735.2; -.  
DR MGD; MGI:1919035; Pdgfd.  
DR InterPro; IPR000859; CUB domain.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00042; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS0278; PDGF 2; 1.  
SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;  
Query Match 42.4%; Score 736; DB 11; Length 370;  
Best Local Similarity 45.6%; Pred. No. 6.9e-64;

Matches 149; Conservative 56; Mismatches 94; Indels 28; Gaps 8;  
QY 10 EONGVQD-POHERIITVSTNGSIHSPRPHTYPRNTLVWRLVAEENVMQLTDFDRFG 68  
Db 42 ESNHLLTDLYQREENIQVTSNGHVQSPRPNSYPRNLLLTWMLRS-QEKTRIQLSFDHQFG 100  
QY 69 LEDPEDDICKYDFVEVEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 126  
Db 101 LEEAENDICRYDFVEVEVSESTVVRGRCWCGHKEIPRITSRTNQIKITFKSDDDYFVAK 160  
QY 127 PGFCIHYNIVMPQFTEAV-----SPSVLPSPSALPLDLNNAITAFST 168  
Db 161 PGFKIYYSFVEDFQPEAASETNWSVSSGVSYSHTDPT-LTADALDKTVAEDT 219  
QY 169 LEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLMLLTVEEVLISCTPRNF 228  
Db 220 VEDLLKHFNFVSWQDDLENLYLDTPHYGRSY-HDKRSK-VDLRLNDDVKRYSCTPRNH 277  
QY 229 SVSTRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKKHYEVLQLRP-- 286  
Db 278 SVNLREELKLTNAVFPFRCCLLVQRCGNCGCGTVNWKSCCTCSSGKTVKKYHEVLKFEFGH 337  
QY 287 -KTGVRGLHKSLLTDVALEHHEECDCVC 312  
Db 338 FRRGKAKNMALVDIQLDHERCDIC 364  
RESULT 13  
Q8K2L3 PRELIMINARY; PRT; 261 AA.  
ID Q8K2L3  
AC Q8K2L3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Similar to platelet-derived growth factor, D polypeptide.  
GN PDGFD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; BC030896; AAH30896.1; -.  
DR MGD; MGI:1919035; Pdgfd.  
DR InterPro; IPR000859; CUB domain.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00042; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
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Query Match 25.0%; Score 434; DB 11; Length 261;  
Best Local Similarity 41.7%; Pred. No. 2.3e-34;  
Matches 93; Conservative 42; Mismatches 64; Indels 24; Gaps 6;  
QY 10 EONGVQD-POHERIITVSTNGSIHSPRPHTYPRNTLVWRLVAEENVMQLTDFDRFG 68  
Db 42 ESNHLLTDLYQREENIQVTSNGHVQSPRPNSYPRNLLLTWMLRS-QEKTRIQLSFDHQFG 100  
QY 69 LEDPEDDICKYDFVEVEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 126  
Db 101 LEEAENDICRYDFVEVEVSESTVVRGRCWCGHKEIPRITSRTNQIKITFKSDDDYFVAK 160  
QY 127 PGFCIHYNIVMPQFTEAV-----SPSVLPSPSALPLDLNNAITAFST 168  
Db 161 PGFKIYYSFVEDFQPEAASETNWSVSSGVSYSHTDPT-LTADALDKTVAEDT 219  
QY 169 LEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDL 211  
Db 220 VEDLLKHFNFVSWQDDLENLYLDTPHYGRSY-HDKRSKGV 261  
Query Match 45.4%; Score 736; DB 11; Length 370;  
Best Local Similarity 42.4%; Pred. No. 6.9e-64;

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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neurophilin-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
RT "Neurophilin-1 is required for normal vascular development and is a
RT mediator of VEGF-dependent angiogenesis in zebrafish.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NEUROPHILIN FAMILY.
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AY064213; AAL40862.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58 C.
DR Pfam; PF00431; CUB; 2.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C.1; 1.
DR PROSITE; PS01286; FA58C.2; 2.
DR PROSITE; PS00740; MAM.1; 1.
DR PROSITE; PS00740; MAM.2; 1.
DR PROSITE; PS00660; MAM_2; 1.
KW Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 923 AA; 102492 MW; 2ED84BL29AA92B2D CRC64;

Query Match 10.6%; Score 184.5; DB 13; Length 923;
Best Local Similarity 30.9%; Pred. No. 4.4e-09;
Matches 60; Conservative 26; Mismatches 87; Indels 21; Gaps 7;

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|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 86 EVRDGVDENGQLVGKYGCKG-IAPSPVSSGNQLFIKFSVD-YETHGAGFSIRYEI FKTGP 143
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QY 195 LLGKAFVFGKRSRV 208
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Search completed: November 25, 2003, 21:04:34
Job time : 29.0774 secs

RESULT 15
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AC Q8AXP1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neurophilin-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
RT "Neurophilin-1 is required for normal vascular development and is a
RT mediator of VEGF-dependent angiogenesis in zebrafish.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NEUROPHILIN FAMILY.
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AY064213; AAL40862.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58 C.
DR Pfam; PF00431; CUB; 2.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C.1; 1.
DR PROSITE; PS01286; FA58C.2; 2.
DR PROSITE; PS00740; MAM.1; 1.
DR PROSITE; PS00740; MAM.2; 1.
DR PROSITE; PS00660; MAM_2; 1.
KW Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 923 AA; 102492 MW; 2ED84BL29AA92B2D CRC64;

Query Match 10.6%; Score 184.5; DB 13; Length 923;
Best Local Similarity 30.9%; Pred. No. 4.4e-09;
Matches 60; Conservative 26; Mismatches 87; Indels 21; Gaps 7;

QY 23 ITVSTNGSIHSPRPHPTYPNTVLVRLVAEENWVLIQTFDERFGLEDPEDDICKYDFV 82
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 29 IRTSANYLTSPGVPVSYPSQKCIWITAPGNQRIILINFNPHFDLEDE---CKYDYV 85
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 83 EVEEPSD--GTILGRWCGSGTVPGKQISKGNQIRIRFVSDVEYFPPSGFCIHYNIVMP-- 138
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Db 86 EVRDGVDENGQLVGKYGCKG-IAPSPVSSGNQLFIKFSVD-YETHGAGFSIRYEI FKTGP 143
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QY 139 ----QFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQ 194
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QY 195 LLGKAFVFGKRSRV 208
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:28:25 ; Search time 3642.09 Seconds  
(without alignments)  
16556.656 Million cell updates/sec

Title: US-09-852-209A-6  
Perfect score: 1474  
Sequence: 1 caccctggagacacagaag.....aatcacaagcactgcacgcg 1474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vi: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1444.8	98.0	2692	10	AF117608	AF117608 Mus muscu
2	1444.8	98.0	3512	10	AF266467	AF266467 Mus muscu
3	1444.8	98.0	3571	6	AR267281	AR267281 Sequence
4	1444.8	98.0	3571	6	AR282985	AR282985 Sequence
5	1444.8	98.0	3571	6	AX044520	AX044520 Sequence
6	1444.8	98.0	3571	6	AX118787	AX118787 Sequence
7	1435.2	97.4	2731	10	BC037696	BC037696 Mus muscu
8	1028.4	69.8	1038	10	AF286725	AF286725 Mus muscu
9	1020.8	69.3	1116	10	AB033830	AB033830 Rattus no
10	914.2	62.0	1817	9	AB033831	AB033831 Homo sapi
11	914.2	62.0	2825	6	AR210624	AR210624 Sequence
12	914.2	62.0	2825	6	AR232022	AR232022 Sequence
13	914.2	62.0	2849	6	AX047650	AX047650 Sequence
14	914.2	62.0	2849	6	AX391260	AX391260 Sequence
15	914.2	62.0	2849	6	AX464152	AX464152 Sequence
16	914.2	62.0	3007	6	AX234498	AX234498 Sequence
17	914.2	62.0	3007	9	AF091434	AF091434 Homo sapi
18	888.2	60.3	2152	9	AF244813	AF244813 Homo sapi
19	882	59.8	1804	6	AX739931	AX739931 Sequence
20	882	59.8	1804	9	AF260738	AF260738 Homo sapi
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22	878.8	59.6	1760	6	AR282949	AR282949 Sequence
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24	878.8	59.6	1760	6	AX118785	AX118785 Sequence
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26	828.6	56.2	1328	6	BD168832	BD168832 Antibody
27	776.4	52.7	1035	6	AX027935	AX027935 Sequence
28	745.8	50.6	1035	6	AR282992	AR282992 Sequence
29	730.8	49.6	774	10	AF508348	AF508348 Rattus no
30	662.4	44.9	1675	5	AB033829	AB033829 Gallus ga
31	660.8	44.8	1035	6	AR282950	AR282950 Sequence
32	519	35.2	918	6	AX119274	AX119274 Sequence
33	355.4	24.1	218449	10	AC122835	AC122835 Mus muscu
34	355.4	24.1	253348	2	AC132143	AC132143 Mus muscu
35	344.8	23.4	504	6	AX027960	AX027960 Sequence
36	343	23.3	1711	10	BC006027	BC006027 Mus muscu
37	283	19.2	110000	2	AC128488	Continuation (3 of
38	283	19.2	250731	2	AC105473	AC105473 Rattus no
39	280.8	19.1	452	6	BD109268	BD109268 EST and e
40	239.4	16.2	213970	2	AC097765	AC097765 Rattus no
41	239.4	16.2	222528	2	AC107118	AC107118 Rattus no
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43	221.8	15.0	152779	2	AC015837	AC015837 Homo sapi
44	216.6	14.7	279	6	AX027968	AX027968 Sequence
45	216.6	14.7	279	6	AX027989	AX027989 Sequence

ALIGNMENTS

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DEFINITION Mus musculus fallotein mRNA, complete cds.  
ACCESSION AF117608  
VERSION AF117608.1 GI:6652867  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 2692)  
REFERENCE  
AUTHORS Tsai, Y.-J., Lee, R.K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W.T.-K.  
TITLE cDNA cloning of fallotein from mouse ovary  
JOURNAL Unpublished



REFERENCE 2 (bases 1 to 2692)  
 AUTHORS Tsai, J.-J., Lee, R. K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W. T.-K.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospital,  
 45 Min Sheng Road, Tamsui, Taipei 25115, Taiwan

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 /evidence=not experimental  
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 /db\_xref="GI:6652868"  
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 SIIMPOVETSPVLPSPSLDLNNAVTFSTLEELIRYLEPRQVLDLSLYK  
 TWLLGKAFLYGKSKVNLMLLKEEVLKYSCTPRNFSVIREELKRTDTIFWPGCLL  
 VKRGGNACCLHNCNECQVPRKVTKKYHEVLQLRPKTKGVKGLKSLTDVALEHHE  
 CDCVCRGNAG"  
 polyA signal  
 2662..2667  
 BASE COUNT 754 a 576 c 617 g 745 t  
 ORIGIN

Query Match 98.0%; Score 1444.8; DB 10; Length 2692;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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 DB 5 AACTGGAGACACAGAGAGGCTCTAGAAAAATTTGGATGGGATATGTGAAACTA 64  
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 DB 125 C-GGCTGGGCTGAGCTTGGAGTCTGCTCTCCAGTCCCGCGGAGTGAGCCCTCG 183  
 QY 182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTCGCGCGGCC 241  
 DB 184 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTCGCGCGGCC 243  
 QY 242 AAGAACGGGACTCGGGCTCAGTCCACCTGAGCAGCAAGTTCAGCTCTCCAGCGACA 301  
 DB 244 AAGAACGGGACTCGGGCTCAGTCCACCTGAGCAGCAAGTTCAGCTCTCCAGCGACA 303  
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 DB 304 AGGAACGAGACGAGTGCAAGATCCCGGCAATGAGAGTGTCTATATCTGGTAATG 363  
 QY 362 GGAGATCCACAGCCCGAGTTTCTCATAGTACCCAGAAATATGCTGCTGGTGGGA 421  
 DB 364 GGAGATCCACAGCCCGAGTTTCTCATAGTACCCAGAAATATGCTGCTGGTGGGA 423  
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 DB 424 GATTAGTTCAGTAGATAAATGTGGATCCAGCTGACATTTGATGAGAGATTTGGGC 483  
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 DB 484 TGGAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTCAGGAGCCCAAGT 543  
 QY 542 ATGGAAGTGTTTAGGAGCTGGTGTGTTCTGGGACTGTGGCAGGAAGCAGACTTCTA 601

544 ATGGAAGCGTTTTAGACCGCTGGTGGTCTGGGACTGTGGCAGGAAACAGACTTCTA 603  
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 DB 604 AAGGAATCATATCAGATAAAGATTGTATCTCATGAGTATTTTCCATCTGAACCCGGAT 663  
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 QY 1082 GTGTCCACCTTAAAGTTTACAAAAAGTACCATGAGTCTCTTCACTTGAGACCAAAAACTG 1141  
 DB 1084 GTGTCCACCTTAAAGTTTACAAAAAGTACCATGAGTCTCTTCACTTGAGACCAAAAACTG 1143  
 QY 1142 GAGTCAAGGATTCATCACTCACTGATGCTGCTGGAACACACAGGAATGTG 1201  
 DB 1144 GAGTCAAGGATTCATCACTCACTGATGCTGCTGGAACACACAGGAATGTG 1203  
 QY 1202 ACTGTGTGTAGAGGAAACGAGGAGGTAACTGTCAGCTTCTGTCAGCAGCAGCTGAG 1261  
 DB 1204 ACTGTGTGTAGAGGAAACGAGGAGGTAACTGTCAGCTTCTGTCAGCAGCAGCTGAG 1263  
 QY 1262 CACTGGCATCTGTGTACCCCAAGCAACCTTTCATCCCAAGCAAGCTTGGCCGAGGG 1321  
 DB 1264 CACTGGCATCTGTGTACCCCAAGCAACCTTTCATCCCAAGCAAGCTTGGCCGAGGG 1323  
 QY 1322 CTCTCAGCTGCTGATGCTGGCTATGGTAAAGATCTTACTGCTCTCCAAACCAATTTCTCAG 1381  
 DB 1324 CTCTCAGCTGCTGATGCTGGCTATGGTAAAGATCTTACTGCTCTCCAAACCAATTTCTCAG 1383  
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 DB 1444 ACCAAGAGGAGTCAATCAAAAGCAGCTGC 1472

## RESULT 2

AF266467

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AF266467 3512 bp mRNA linear ROD 02-JUN-2001  
 Mus musculus platelet-derived growth factor C (Pdgfr) mRNA,  
 complete cds.  
 AF266467  
 AF266467.1 GI:14279331  
 Mus musculus (house mouse)



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3512) Gao, Z., Hart, C., Piddington, C., Sheppard, P., Shoemaker, K., Gilbertson, D., West, J. and O'Hara, P.J. Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor Unpublished 2 (bases 1 to 3512) Gao, Z., Hart, C., Piddington, C., Sheppard, P., Shoemaker, K., Gilbertson, D., West, J. and O'Hara, P.J. Direct Submission Submitted (10-MAY-2000) Biomedical Informatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA FEATURES Location/Qualifiers 1..3512 /organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J" /db\_xref="taxon:10090" 1..3512 /gene="Pdgfc" 1022..2059 /gene="Pdgfc" /note="PDGF-C/ZVEGF3" /codon\_start=1 /product="platelet-derived growth factor C" /protein\_id="AAK58566.1" /db\_xref="GI:14279332" /translation="MLILGLLLLSALAGQRTGRASNLSSKLQLSDKEQGVQDP RHEVVTISNGSITHSPKPHYPRNMVLVRLVAVDENVRILQIFDERGLEPDD ICKYDFVEBPSDGLRWCGSGTVPKGTSGNHRIRFVSDSEYFPSPGDIHY SIIMPOVTEPSPVLPPSLSLDLNNAVTAFLBELIRLPLPDRWQVLDLSLYP TWILGKAFLYKSKVKNLLKKEVKLYSTPRNFSVSIRELKRDTDTFWPGCLL VKRCGNCAACCLHNCQCQVPRVTKYHVEVLQRLPKTVGKGLHLSLTDVALEHHE CDCVCRGNAGG" BASE COUNT 850 a 920 c 861 g 881 t ORIGIN Query Match 98.0%; Score 1444.8; DB 10; Length 3512; Best Local Similarity 99.4%; Pred. No. 0; Mismatches 1; Gaps 1; Matches 1460; Conservative 0; 2 ACCTGGACACACAGAGGGCTCTAGGAAAATTTGGATGGGATTAATGTGGAACCTA 61 829 AACTGGAACACAGAGGGCTCTAGGAAAATTTGGATGGGATTAATGTGGAACCTA 888 62 CCCTGCGATTCTCTGCGACAGCGCGCGAGCGCTTCCACCGACGCGACCTTTCC 121 889 CCCTGCGATTCTCTGCGACAGCGCGCGAGCGCTTCCACCGACGCGACCTTTCC 948 122 CGGCTGGGCTGAGCTTGGAGTGTCTGCTTCCCGAGTCCCGCGCGAGTGGAGCTCG 181 949 C-GGCTGGGCTGAGCTTGGAGTGTCTGCTTCCCGAGTCCCGCGCGAGTGGAGCTCG 1007 182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTGCTGACATCTGCTTGGCGCGGC 241 1008 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTGCTGACATCTGCTTGGCGCGGC 1067 242 AAAGAACGGGGAATGCGGCTGAGTCCAACTGAGCGAGGAGTTCAGCTCTCCAGGACA 301 1068 AAAGAACGGGGAATGCGGCTGAGTCCAACTGAGCGAGGAGTTCAGCTCTCCAGGACA 1127 302 AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGTGTCTACTATATCTGGTAATG 361 1128 AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGTGTCTACTATATCTGGTAATG 1187 362 GGAGCATCCACAGCCGAGATTTCTCTATACGTACCCAGAAATATGGTGTGTGGA 421 1188 GGAGCATCCACAGCCGAGATTTCTCTATACATACCCAGAAATATGGTGTGTGGA 1247 422 GATTAGTTCAGTAGAATAATGTGGGATCCAGCTGACATTTGATGAGATTTGGGC 481

1248 GATTAGTTCAGTAGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1307 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 541 1308 TGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 1367 542 ATGGAAGTGTTTAGAGCGCTGGTGGTCTTGGGACTGTGCCAGGAAAGCAGACTTCTA 601 1368 ATGGAAGTGTTTAGAGCGCTGGTGGTCTTGGGACTGTGCCAGGAAAGCAGACTTCTA 1427 602 AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTCAACCCGAT 661 1428 AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTCAACCCGAT 1487 662 TCTGCATCCACTACAGTATTATCATGCCAAGAATGTCACAGAAACACAGATCCTTCGGTGT 721 1488 TCTGCATCCACTACAGTATTATCATGCCAAGAATGTCACAGAAACACAGATCCTTCGGTGT 1547 722 TGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACATGCTGCTGACCTGCCTTCAGTACT 781 1548 TGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACATGCTGCTGACCTGCCTTCAGTACT 1607 782 TGAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGACCTTGGACAGCTCT 841 1608 TGAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGACCTTGGACAGCTCT 1667 842 ACAAGCAACATGCGAGCTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901 1668 ACAAGCAACATGCGAGCTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1727 902 TGAATCTGAATCTCTCAAGAGAGGTAACACTCTACAGCTGCACACCCCGAACTTCT 961 1728 TGAATCTGAATCTCTCAAGAGAGGTAACACTCTACAGCTGCACACCCCGAACTTCT 1787 962 CAGTGTCCATACCGGAGAGCTAAAGAGACAGATACCATATTTCTGGCAGGTTGTCTCC 1021 1788 CAGTGTCCATACCGGAGAGCTAAAGAGACAGATACCATATTTCTGGCAGGTTGTCTCC 1847 1022 TGGTCAAGCGCTGTGGAGAAATTTGTGCTCTCAATATTTGCAATGTAATGTCACT 1081 1848 TGGTCAAGCGCTGTGGAGAAATTTGTGCTCTCAATATTTGCAATGTAATGTCACT 1907 1082 GTGTCCCAAGTAAAGTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACCTG 1141 1908 GTGTCCCAAGTAAAGTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACCTG 1967 1142 GAGTCAAGGGATTGCTAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 1201 1968 GAGTCAAGGGATTGCTAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 2027 1202 ACTGTGTGTAGAGGAAACGAGAGGATACTGAGCGCTTTCGTAGCAGCACAAGTGTAG 1261 2028 ACTGTGTGTAGAGGAAACGAGAGGATACTGAGCGCTTTCGTAGCAGCACAAGTGTAG 2087 1262 CACTGGCATCTGTGTACCCCAAGCAACCTTCACTCCCAAGCAGCGTTGGCCGAGG 1321 2088 CACTGGCATCTGTGTACCCCAAGCAACCTTCACTCCCAAGCAGCGTTGGCCGAGG 2147 1322 CTCTCAGTGTCTGATGTGGCTATGTAAAGATCTTACTCTCTCCAAACCAAAATCTCAG 1381 2148 CTCTCAGTGTCTGATGTGGCTATGTAAAGATCTTACTCTCTCCAAACCAAAATCTCAG 2207 1382 TTGTTTGTCTCAATAGCCTTCCCTGAGGACTTCAAGTGTCTTCTTAAAGACAGAGGC 1441 2208 TTGTTTGTCTCAATAGCCTTCCCTGAGGACTTCAAGTGTCTTCTTAAAGACAGAGGC 2267 1442 ACCAAGAGGATCAATCACAAGGACTGC 1470 2268 ACCAAGAGGAGTCAATCACAAGGACTGC 2296

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DEFINITION Sequence 34 from patent US 6495668.  
ACCESSION AR267281  
VERSION AR267281.1 GI:29697284  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3571)  
AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.  
TITLE Growth factor homolog ZVEGF4  
JOURNAL Patent: US 6495668-A 34 17-DEC-2002;  
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LOCUS AR282985 3571 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 42 from patent US 6528050.  
ACCESSION AR282985  
VERSION AR282985.1 GI:29719806  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3571)  
AUTHORS Gao, Z., Hart, C.E., Piddington, C.S., Sheppard, P.O., Shoemaker, K.E.,  
Gilbertson, D.G. and West, J.W.  
TITLE Growth factor homolog zvegf3  
JOURNAL Patent: US 6528050-A 42 04-MAR-2003;  
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BASE COUNT 876 a 935 c 875 g 885 t  
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Query Match 98.0%; Score 1444.8; DB 6; Length 3571;  
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ACCESSION	AX044520											
VERSION	AX044520.1 GI:11343375											
KEYWORDS	Mus musculus (house mouse)											
SOURCE	Mus musculus											
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.											
REFERENCE	1 Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.											
AUTHORS	Growth factor homolog zvegf4											
TITLE	Patent: WO 0066736-A 34 09-NOV-2000;											
JOURNAL	ZymoGenetics, Inc. (US)											
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Query Match	98.0%; Score 1444.8; DB 6; Length 3571;											
Best Local Similarity	99.4%; Pred. No. 0;											
Matches 1460; Conservative	0; Mismatches 8; Indels 1; Gaps 1;											
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ACCESSION AX118787  
VERSION AX118787.1 GI:14035736  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS Gilbertson,D.G.  
TITILE Method of treating fibrosis  
JOURNAL Patent: WO 0128586-A 3 26-APR-2001;  
ZymoGenetics, Inc. (US)  
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## RESULT 7

BC037696 2731 bp mRNA linear ROD 16-APR-2003  
LOCUS BC037696  
DEFINITION Mus musculus platelet-derived growth factor, C polypeptide, mRNA  
(cDNA clone MGC:46836 IMAGE:4008749), complete cds.

ACCESSION BC037696

VERSION BC037696.1 GI:22902442

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2731)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zesberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,  
Villalón, D.K., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2731)

Strausberg, R.

Direct Submission

Submitted (13-SEP-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contract: MGC help desk

Email: [cgabs-t@mail.nih.gov](mailto:cgabs-t@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

cDNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc\_mgc@nhgri.nih.gov

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lari, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripol, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN at: <http://image.llnl.gov>  
Series: IRAC Plate: 80 Row: f Column: 13  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10242384.

## FEATURES

source

Location/Qualifiers

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1	Hamada, T., Ui-Tei, K., Imaki, J., and Miyata, Y.	Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotsein	Biochem. Biophys. Res. Commun.	280 (3), 733-737 (2001)		1	Hamada, T., Ui-Tei, K., and Miyata, Y.	Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/fallotsein	Biochem. Biophys. Res. Commun.		
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11625582						11625582					
2	(bases 1 to 1116)					2	(bases 1 to 1116)				
1	Hamada, T., Ui-Tei, K. and Miyata, Y.	Direct Submission				1	Hamada, T., Ui-Tei, K. and Miyata, Y.	Direct Submission			
Submitted (25-OCT-1999)						Submitted (25-OCT-1999)					
Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo						Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo					
113-8602, Japan (E-mail: t-hamada@rms.ac.jp, Tel:81-3-3822-2131 (ex.5277), Fax:81-3-584-1684)						113-8602, Japan (E-mail: t-hamada@rms.ac.jp, Tel:81-3-3822-2131 (ex.5277), Fax:81-3-584-1684)					
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Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo  
113-8602, Japan (E-mail: t-hamada@nms.ac.jp,  
Tel: 81-3-3822-2131 (ex. 5277), Fax: 81-3-5814-1684)

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SOURCE Unknown.  
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REFERENCE 1 (bases 1 to 2825)  
AUTHORS Ferrara,N. and Kuo,S.S.  
TITLE Polypeptides having homology to vascular endothelial cell growth factor and bone morphogenetic protein 1  
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ACCESSION AR232022  
VERSION AR232022.1 GI:27273902  
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REFERENCE 1 (bases 1 to 2825)  
AUTHORS Ferrara, N. and Kuo, S.S.  
TITLE Nucleic acids encoding vascular endothelial cell growth factor-E (VEGF-E)  
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 AUTHORS  
 Baker,K.P., Chen,J., Ferrara,N., Fong,S., Goddard,A., Gurney,A.L.,  
 Hillan,K.J., Kuo,S.S., Tumas,D. and Wood,W.I.  
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 Compositions and methods for the treatment of immune related  
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 Patent: WO 0070050-A 9 23-NOV-2000;  
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VERSION	AX391260.1	GI:196999933	
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AUTHORS	Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marsters, S.A., Patti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni, N.F., and Watanabe, C.K.		
TITLE	Promotion or inhibition of angiogenesis and cardiovascularization		
JOURNAL	Patent: WO 0073445-A 3 07-DEC-2000;		
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Db	147	CCCTGGCAATTCCTGCTCCAGAGCGAGCTCGGGCTTCCACCCGACGCGACCTTTC	206
Qy	122	CGG----GCTGGGTGAGCCCTTGGAGTCTGCTTCCCTTCCAGTGGCCGCGAGTGAGCC	177
Db	207	TGGCGGTGGTGAAGAGACTCGGAGTCTGCTTCCAAAGTCCCGCGTGGTGGT	266
Qy	178	CTCGCCCAAGTACAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCGCTG	237
Db	267	CTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTGACATCTGCGCTG	326
Qy	238	GGCCCAAGAAACGGGACTCGGGCTGAGTCCCAACCTGACGACCAAGTTCAGCTCTCC	297
Db	327	GGCCCAAGAAACGGGACTCGGGGAAATCCCAACCTGAGTGAATTCAGTTTTCACG	386
Qy	298	GACAGGAAACAGACGGAGTGCAGATCCCGGCAATGAGAGTGTGCTATATCTGCT	357
Db	387	AACAGGAAACAGACGGAGTGCAGATCTCAGCATGAGAAATTAATTAATCTGCTACT	446
Qy	358	AATGGGAGCATCCACAGCCCGAAGTTTCCTCATAGTACCCAGAAATATGCTGCTGTG	417

Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Wood, W.L. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
same

JOURNAL Patent: WO 0140466-A 285 07-JUN-2001;  
Genentech Inc. (US)

FEATURES Location/Qualifiers

1..2849  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 851 a 528 c 619 g 850 t 1 others

Query Match	62.0%;	Score 914.2;	DB 6;	Length 2849;
Best Local Similarity	83.5%;	Pred. No. 7e-255;	Mismatches 203;	Indels 4; Gaps 1;
Matches 1050;	Conservative	0;		
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTATGTGGAACCTA	61	
Db	87	AACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTATGTGGAACCTA	146	
QY	62	CCCTGGATTCTGTGTCAGAGCCGCGCAGCGCTTCACCGCAGCGCAGCTTTCCC	121	
Db	147	CCCTGGATTCTGTGTCAGAGCGGCTCGCGCTTCACCCAGTCAGCGCTTTCCC	206	
QY	122	CGS- -GCTGGGCTGAGCTTGGAGTCTGTGCTTCCCGAGTCCCGCGCAGTGAAGC	177	
Db	207	TGGCGGTGTGAAGAGATCTGGGAGTCTGTGCTTCCAAAGTCCCGCGTGAAGT	266	
QY	178	CTCGCCCGCAGTCCAGCAATGCTCTCTCGGCTCTCTGTGACATCTGCTCGGCC	237	
Db	267	CTCACCCAGTCAGCCAAATGAGCCTTTCGGGCTTCTCTGTGACATCTGCGCTGGCC	326	
QY	238	GGCAGAGAACGGGACTCGGCTGAGTCCAACTGAGCAGCAGTTCAGCTCTCCAGC	297	
Db	327	GGCAGAGAACGGGACTCGGCGGAATCCAACTGAGTAGTAATTTCCAGTTTTCAGC	386	
QY	298	GACAGGAACAGAACGGAGTGCAGAGTCCCGCATGAGAGTGTCTACTATCTGGT	357	
Db	387	AACAGGAACAGAACGGAGTACAGATCTCTGACATGAGAGATTTACTGTGCTACT	446	
QY	358	AATGGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAGAAATATGGTGGTG	417	
Db	447	AATGGAAGTATTCACAGCCCAAGTTTCTCTACTATTCACAGAAATACGGTCTTGTA	506	
QY	418	TGAGATTAGTTGACGTAGATGAATATGCGGATCCAGCTGACATTTGATGAGATTT	477	
Db	507	TGAGATTAGTACGACGTAGAGGAATATGATGGATACAACTTACGTTTGAATGAAGATT	566	
QY	478	GGCTGGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCC	537	
Db	567	GGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCC	626	
QY	538	AGTATGGAAGTGTTTTAGGACGCTGGTGTGGTTCTGGGACTGTGCCAGAAAGCAGCT	597	
Db	627	AGTATGGAAGTATATTAGGGCTGTGGTGTGGTTCTGGTACTGTACCCAGGAAACAGATT	686	
QY	598	TCTAAGGAATCATATCAGGATAAGATTGTATCTGATGAGTATTTCCATCTGAACCC	657	
Db	687	TCTAAGGAATCAATATTAGGATAAGATTGTATCTGATGAGTATTTTCTCTGAACCA	746	
QY	658	GGATTCTGATCCACTACAGTATATATCATGCCAAGTCACAGAAACCAAGTCTCTTCG	717	
Db	747	GGTTTCTGATCCACTACAGTATGTCGCCAATTCACAGAGCTGTGAGTCTCTCA	806	
QY	718	GTGTTGCCCTTCTATCTTTGTCATTTGACCTGCTCAACAAATGCTGTGACTGCTTCAGT	777	
Db	807	GTGCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATAATGCTATTAAGTCTTAGT	866	
QY	778	ACCTTGGAGAGCTGATTCGGTACCTAGACGAGATCGATGGCAGGTGGACTTGGACAGC	837	
Db	867	ACCTTGGAGAGCTTATTCGATATCTTTGAACACAGAGAGATGGCAGGTGGACTTGAAGAT	926	

QY	838	CTCTACAGCCCAACATGGCAGCTTTTGGCAAGGCTTTCTGTATGGGAAAAAAGCAAA	897	
Db	927	CTATATAGCCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTAAGAAATCCAGA	986	
QY	898	GTGGTGAATCTGAATCTCTCAAGGAGAGGTAATAACTCTACAGCTGCACACCCCGAAC	957	
Db	987	GTGGTGAATCTGAACCTTCTAAACAGAGGAGTAAGATTATACAGCTGCACACCTCGTAAC	1046	
QY	958	TTCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT	1017	
Db	1047	TTCTCAGTGTCCATTAAGGGAAGACTTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGT	1106	
QY	1018	CTCTGGTCAAGCGCTGTGGAGAAATTTGTGCTGTGTCTCCATTAATTGCAATGAATGT	1077	
Db	1107	CTCTGGTTAAACGCTGTGTGGAACTCTGCTGTGTGCTCCCAATTTGCAATGAATGT	1166	
QY	1078	CAGTGTGTCCCACTGAATTTACAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAA	1137	
Db	1167	CAATGTGTCCCAAGCAAAAGTTACTAAAAAATACACGAGTCTCTCAGTTGAGACCAAG	1226	
QY	1138	ACTGGAGTCAAGGGATTGCATTAAGTCACTCACTGTGTGCTCTGGAACACACACGAGAA	1197	
Db	1227	ACCGTGTCAAGGGATTGCATTAATCACTCACTGACGCTGCTGAGACCATGAGGAG	1286	
QY	1198	TGTGACTGTGTGTAGAGGAAACGAGGAGGTAATCTGAGCGCTTCTGTAGCAGCAC	1254	
Db	1287	TGTGACTGTGTGTAGAGGAGCACAGGAGGATAGCCGATCACCACACGAGCAGCTC	1343	

Search completed: November 26, 2003, 03:42:42  
Job time : 3647.09 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:26:15 ; Search time 272.163 Seconds  
(without alignments)

14619.814 Million cell updates/sec

Title: US-09-852-209A-6

Perfect score: 1474

Sequence: 1 cactcgagacacagaag.....aatcacaagcactgcacgc 1474

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03.\*

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25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1473	99.9	1474	21	AA12525
2	1444.8	98.0	3571	21	AA12525
3	1444.8	98.0	3571	21	AA12525
4	1444.8	98.0	3571	22	AA12525
5	1444.8	98.0	3571	24	AB92668
6	1444.8	98.0	3571	24	AA17244
7	1444.8	98.0	3571	25	AB92668
8	914.2	62.0	1473	21	AA171955

9	914.2	62.0	2632	24	ABQ81461
10	914.2	62.0	2668	21	AA171990
11	914.2	62.0	2825	20	AA223691
12	914.2	62.0	2825	25	AB57294
13	914.2	62.0	2827	22	AA06812
14	914.2	62.0	2839	21	AA17452
15	914.2	62.0	2849	20	AA234296
16	914.2	62.0	2849	21	AA278582
17	914.2	62.0	2849	21	AA188515
18	914.2	62.0	2849	21	AA188515
19	914.2	62.0	2849	21	AA177621
20	914.2	62.0	2849	22	AA21386
21	914.2	62.0	2849	22	AA20564
22	914.2	62.0	2849	22	AA20564
23	914.2	62.0	2849	22	AA20564
24	914.2	62.0	2849	25	AA03745
25	914.2	62.0	2849	25	AA04166
26	914.2	62.0	2849	25	AB92668
27	914.2	62.0	2849	25	AB92668
28	914.2	62.0	2896	21	AA24426
29	914.2	62.0	2898	20	AA24426
30	914.2	62.0	3007	22	AA12884
31	912.6	61.9	2779	21	AA24426
32	911	61.8	2858	21	AA24426
33	895.8	60.8	2776	21	AA171952
34	878.8	59.6	1760	21	AA18314
35	878.8	59.6	1760	21	AA18314
36	878.8	59.6	1760	22	AA04649
37	878.8	59.6	1760	24	AB56812
38	878.8	59.6	1760	24	AA17244
39	878.8	59.6	1760	25	AB92668
40	842.8	57.2	3087	21	AA18314
41	837.6	56.8	2475	21	AA171951
42	828.6	56.2	1328	22	AA18259
43	828.6	56.2	1328	24	ABN8974
44	815.4	55.3	2794	21	AA24426
45	810.8	55.0	2108	21	AA12525

#### ALIGNMENTS

RESULT 1  
AA12525  
ID AA12525 standard; cDNA; 1474 BP.

AC AA12525;

XX 25-JUL-2000 (first entry)

DT cDNA encoding murine platelet-derived growth factor C (PDGF-C).

DE cDNA encoding murine platelet-derived growth factor C (PDGF-C).

XX platelet-derived growth factor C; PDGF-C; cell proliferation;

KW growth factor; heparin; connective tissue; wound healing; VEGF-F;

KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;

KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;

XX lung carcinoma; erythroleukemia; tissue remodelling; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 196..1233

FT FT /\*tag= a

FT FT /product= "platelet-derived growth factor C"

XX WO200018212-A2.

XX PD 06-APR-2000.

XX PF 30-SEP-1999; 99WO-US22668.

XX PR 30-SEP-1998; 98US-0102461.

PR 12-NOV-1998; 98US-0108109.





XX	Sequence	3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
SQ	Query Match	98.0%; Score 1444.8; DB 21; Length 3571;
	Best Local Similarity	99.4%; Pred. No. 0;
	Matches 1460; Conservative	0; Mismatches 8; Indels 1; Gaps 1;
QY	2	ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGGATTTATGTGGAAACTA 61
DB	856	AAC TGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGGATTTATGTGGAAACTA 915
QY	62	CCCTGCGATTTCTTGTGCGAGAGCGCGCCAGGCGCTTCCACCGCAGCGACGCTTTTCCC 121
DB	916	CCCTGCGATTTCTTGTGCGAGAGCGCGCCAGGCGCTTCCACCGCAGCGACGCTTTTCCC 975
QY	122	CGGCTGGGCTGAGCCTTTGGAGTGGTCCCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 181
DB	976	C-GGCTGGGCTGAGCCTTTGGAGTGGTCCCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 1034
QY	182	CCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATGTCCTCGGCGCGCC 241
DB	1035	CCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATGTCCTCGGCGCGCC 1094
QY	242	AAAGAACCGGACTCGGCTGAGTCCAACTCAGCAGCAAGTTGCGAGCTCTCCAGCGACA 301
DB	1095	AAAGAACCGGACTCGGCTGAGTCCAACTCAGCAGCAAGTTGCGAGCTCTCCAGCGACA 1154
QY	302	AGGAACAGAACGGAGTGCAGATCCCGGCATGAGAGAGTTGTCATATATCTGGTAATG 361
DB	1155	AGGAACAGAACGGAGTGCAGATCCCGGCATGAGAGAGTTGTCATATATCTGGTAATG 1214
QY	362	GGAGCATCCACAGCCCGAAGTTTCTCATACCTA CCAAGAAATATGGTGTGTTGTGGA 421
DB	1215	GGAGCATCCACAGCCCGAAGTTTCTCATACCTA CCAAGAAATATGGTGTGTTGTGGA 1274
QY	422	GATTAGTTGCAATGATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481
DB	1275	GATTAGTTGCAATGATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334
QY	482	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTCTAGAAAGTTGAGGAGCCAGTG 541
DB	1335	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTCTAGAAAGTTGAGGAGCCAGTG 1394
QY	542	ATGGAAGTGTTTTAGGACGCTGTTGTTCTGGACTGTGCGAGCTGTCAGAAAGCAGACTCTA 601
DB	1395	ATGGAAGTGTTTTAGGACGCTGTTGTTCTGGACTGTGCGAGCTGTCAGAAAGCAGACTCTA 1454
QY	602	AAGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCGGAT 661
DB	1455	AAGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCGGAT 1514
QY	662	TCTGCATCCACTACAGTATTTATCATGCCACAAGTCCAGAAACCAAGAGTCCTTCGGTGT 721
DB	1515	TCTGCATCCACTACAGTATTTATCATGCCACAAGTCCAGAAACCAAGAGTCCTTCGGTGT 1574
QY	722	TGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACAAATGCTGTGAGCTGTCAGTACCT 781
DB	1575	TGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACAAATGCTGTGAGCTGTCAGTACCT 1634
QY	782	TGGAAGCTGATTCCGTACCTAGACCCAGATCGATGGCAGGTGGATCTGAGACGCTCT 841
DB	1635	TGGAAGCTGATTCCGTACCTAGACCCAGATCGATGGCAGGTGGATCTGAGACGCTCT 1694
QY	842	ACAAGCCCAATCGGACGCTTTTGGGCAAGGCTTCTCTGTATGGAAAAAAGCAAGTGG 901
DB	1695	ACAAGCCCAATCGGACGCTTTTGGGCAAGGCTTCTCTGTATGGAAAAAAGCAAGTGG 1754
QY	902	TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTCT 961
DB	1755	TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTCT 1814
QY	962	CAGTGTCCATACCGGAAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTCC 1021

RESULT 2  
ID AAC81583 standard; DNA; 3571 BP.  
AC AAC81583;  
XX 09-MAR-2001 (first entry)  
XX Mouse zvegf3 DNA, SEQ ID NO:34.  
XX Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;  
KW murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;  
KW neovascularisation; tissue repair; proliferation; differentiation;  
KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;  
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
KW immunomodulation; hepatic; ds.  
XX OS Mus musculus.  
XX WO2000066736-A1.  
XX 09-NOV-2000.  
XX 03-MAY-2000; 2000WO-US40047.  
XX 03-MAY-1999; 99US-0304216.  
PR 10-NOV-1999; 99US-0164463.  
PR 04-FEB-2000; 2000US-0180169.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
PI WPI; 2000-687541/67.  
DR P-PSDB; AAB48658.  
XX Growth factor homologs and the nucleic acids that encode them, useful  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease -  
XX Disclosure; Page 127-130; 143pp; English.  
PS The invention relates to the human growth factor homologue zvegf4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zvegf4 has a growth factor domain (AAB48654)  
CC characterised by a PDGF cysteine knot structure, and a CUB domain  
CC (AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like  
CC activity, having mitogenic activity on fibroblasts, vascular smooth  
CC muscle cells and pericytes, and has also been shown to stimulate bone  
CC growth. The invention also relates to fusion proteins comprising human  
CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3  
CC fusions; expression constructs and host cells comprising human zvegf4  
CC nucleic acids; the recombinant expression of human zvegf4; an antibody  
CC which binds to human zvegf4 or a fragment thereof; a method of activating  
CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a  
CC method of modulating the proliferation, differentiation, migration or  
CC metabolism of bone cells, comprising exposing bone cells to  
CC zvegf4-derived polypeptides; and a method of detecting a genetic  
CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived  
CC fragments may be used to stimulate tissue development or repair, or  
CC cellular differentiation or proliferation. They are particularly used for  
CC the treatment or repair of liver damage, and may also be used to  
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
CC multiple sclerosis). Due to their osteogenic activity, they may be used  
CC in the treatment of periodontal disease and fractures. They may also be  
CC used to enhance expansion and mobilisation of haematopoietic stem cells  
CC and endothelial precursor stem cells, which may be useful in the  
CC treatment of ischaemia, in wound healing, and in the modulation of the  
CC immune system. The present sequence represents DNA encoding mouse  
CC zvegf3.



Db 1815 CAGTGTCCATACGGGAAGAGCTAAGAGGACAGATACATATCTGGCCAGTTGTCTCC 1874  
Qy 1022 TGGTCAAGCGCTGTGGAGGAATTTGGCTGTTTCTTCCATAATTCGAATGTCAGT 1081  
Db 1875 TGGTCAAGCGCTGTGGAGGAATTTGGCTGTTTCTTCCATAATTCGAATGTCAGT 1934  
Qy 1082 GTGTCCACAGTAAAGTTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACGTG 1141  
Db 1935 GTGTCCACAGTAAAGTTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACGTG 1994  
Qy 1142 GAGTCAAGGATTCATAAGTCACTCACTGATGTGGTCTTGGAAACACACAGGAATGTG 1201  
Db 1995 GAGTCAAGGATTCATAAGTCACTCACTGATGTGGTCTTGGAAACACACAGGAATGTG 2054  
Qy 1202 ACTGTGTGTAGAGGAACGAGAGGTAACCTGACGCTTCGTAGCAGCACAGTGTAG 1261  
Db 2055 ACTGTGTGTAGAGGAACGAGAGGTAACCTGACGCTTCGTAGCAGCACAGTGTAG 2114  
Qy 1262 CACTGGCATTCTGTGTACCCCAAGCAACCTTCATCCCAACAGCGTTGGCCGACGG 1321  
Db 2115 CACTGGCATTCTGTGTACCCCAAGCAACCTTCATCCCAACAGCGTTGGCCGACGG 2174  
Qy 1322 CTCTCAGCTGCTGATGTGGTATGTTAAAGATCTTACTGCTTCCAAACCAAAATCTCAG 1381  
Db 2175 CTCTCAGCTGCTGATGTGGTATGTTAAAGATCTTACTGCTTCCAAACCAAAATCTCAG 2234  
Qy 1382 TGTGTTGCTTCAATAGCTTCCCTGCGAGGCTTCAAGTGCTTCTTAAAGACCAAGGCG 1441  
Db 2235 TGTGTTGCTTCAATAGCTTCCCTGCGAGGCTTCAAGTGCTTCTTAAAGACCAAGGCG 2294  
Qy 1442 ACCAAGAGGATCAATCAAGCACTGC 1470  
Db 2295 ACCAAGAGGATCAATCAAGCACTGC 2323

RESULT 3  
AAA51527  
ID AAA51527 standard; cDNA; 3571 BP.  
XX  
AC AAA51527;  
XX

26-SEP-2000 (first entry)

DE Murine vascular endothelial growth factor homologue, ZVEGF3 DNA.  
XX  
DE Vascular endothelial growth factor; homologue; zvegf3; CUB domain;  
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;  
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;  
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;  
KW vulnery; ss.  
XX  
OS Mus musculus.

XX Key Location/Qualifiers  
FH 1049..2086  
CDS /\*tag= a  
FT /product= ZVEGF3  
FT

XX W0200034474-A2.

XX 15-JUN-2000.

XX 07-DEC-1999; 99MO-US28968.

XX 07-DEC-1998; 98US-0207120.

PR 06-JUL-1999; 99US-0142576.

PR 21-OCT-1999; 99US-0161653.

PR 12-NOV-1999; 99US-0165255.

XX (ZYMO ) ZYMOGENETICS INC.

XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
PI Gilbertson DG, West JW;

XX WPI; 2000-423420/36.  
DR P-PSDB; AAY96861.  
XX  
PT Novel zvegf3 polypeptides and nucleotides encoding them useful for  
PT stimulating growth of smooth muscle cells and fibroblasts comprising an  
PT epitope bearing portion of a specific amino acid sequence  
XX  
PS Claim 30; Page 166-169; 173pp; English.  
XX  
CC This DNA encodes murine ZVEGF3 a novel vascular endothelial growth  
CC factor homologue. Polypeptides comprising an epitope-bearing portion  
CC human or murine ZVEGF3 are claimed. The growth factors comprise a growth  
CC factor domain and a CUB domain (generic sequence motifs are shown in  
CC AAY96859 and AAY96860). The growth factor domain is characterized by an  
CC arrangement of cysteine residues and beta-strands that is characteristic  
CC of the "cysteine knot" structure of the platelet-derived growth factor  
CC (PDGF) family. The CUB domain shows homology to CUB domains in  
CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma  
CC protein, bovine acidic seminal fluid protein and Xenopus laevis  
CC tolloid-like protein. Structural analysis and homology predict that  
CC ZVEGF3 polypeptides complex with a second polypeptide to form multimeric  
CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.  
CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth  
CC muscles cells, for activating cell surface PDGF-alpha receptor and for  
CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is  
CC useful for regulating (post-development) organ growth, regeneration and  
CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3  
CC antagonists are useful for treating cancer, rheumatoid arthritis,  
CC diabetic retinopathy, ischemic limb disease, peripheral vascular  
CC disease, myocardial ischemia, vascular intimal hyperplasia,  
CC atherosclerosis, wound healing, chronic liver disease and haemangioma  
CC formation. ZVEGF3 can also be used to modulate neurite growth and  
CC development of the nervous system, and for treating neurodegenerative  
CC diseases.

XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match 98.0%; Score 1444.8; DB 21; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
Qy 2 ACCTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGGAAACTA 61  
Db 856 AACTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGGAAACTA 915  
Qy 62 CCTCGGATTCCTCTGCGCAGCGCGCCGCGCTTCCACCGCAGCGCAGCTTTTCCC 121  
Db 916 CCTCGGATTCCTCTGCGCAGCGCGCCGCGCTTCCACCGCAGCGCAGCTTTTCCC 975  
Qy 122 CGGGCTGGGCTGAGCCTTGGAGTCGTCCTTCCCAAGTCCCGCCGCGAGTGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCTTGGAGTCGTCCTTCCCAAGTCCCGCCGCGAGTGAGCCCTCG 1034  
Qy 182 CCCCAGTCAGCCAAATGCTTCTTCCGCTCTCTCTGTCGACATCTGCCCTGGCCGCC 241  
Db 1035 CCCCAGTCAGCCAAATGCTTCTTCCGCTCTCTCTGTCGACATCTGCCCTGGCCGCC 1094  
Qy 242 AAAGACGGGGACTCGGGCTGAGTCCAACTCAGCAGCAAGTTTGCAGCTCTCCAGCGACA 301  
Db 1095 AAAGACGGGGACTCGGGCTGAGTCCAACTCAGCAGCAAGTTTGCAGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACCGAGTGCAGATATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 361  
Db 1155 AGGAACAGAACCGAGTGCAGATATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214  
Qy 362 GGAGCATCCACAGCCCGGAATGTTTCTTCATACGTACCCAGAAATATGGTGTGTGGA 421  
Db 1215 GGAGCATCCACAGCCCGGAATGTTTCTTCATACGTACCCAGAAATATGGTGTGTGGA 1274  
Qy 422 GATTAGTTCAGTGTAGTGAATGTGCGGATCCAGCTCCAGCTTGATGAGAGATTTGGGC 481  
Db 1275 GATTAGTTCAGTGTAGTGAATGTGCGGATCCAGCTTGATGAGAGATTTGGGC 1334

QY 482 TGGAGATCCAGACGATATATGCAAGTAGTATGTTTGTAGAGTTGAGGAGCCAGTG 541  
Db 1335 TGGAGATCCAGACGATATATGCAAGTAGTATGTTTGTAGAGTTGAGGAGCCAGTG 1394  
QY 542 ATGGAAGTGTATTTAGGACGCTGGTGTGTTTGGGACCTGTGCGAGGAAAGCAGACTTCTA 601  
Db 1395 ATGGAAGTGTATTTAGGACGCTGGTGTGTTTGGGACCTGTGCGAGGAAAGCAGACTTCTA 1454  
QY 602 AAGGAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCGGAT 661  
Db 1455 AAGGAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCGGAT 1514  
QY 662 TCTGCATCCATACAGTATTTATCATGCCCAAGTACAGAAACCCAGAGTCTCTTGGGTGT 721  
Db 1515 TCTGCATCCATACAGTATTTATCATGCCCAAGTACAGAAACCCAGAGTCTCTTGGGTGT 1574  
QY 722 TGCCTCCCTTCATCTTTGTGATTTGGACCTGCTCAACAATCTGTGACTGCTTCAGTACT 781  
Db 1575 TGCCTCCCTTCATCTTTGTGATTTGGACCTGCTCAACAATCTGTGACTGCTTCAGTACT 1634  
QY 782 TGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGCTCT 841  
Db 1635 TGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGCTCT 1694  
QY 842 ACAAGCCATCATGGCAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCATCATGGCAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGAATCTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGAATCTCT 1814  
QY 962 CAGTGTCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1074  
QY 1022 TGTCAAGCGCTGTGAGGAAATTTGTCCCTGTTGTCTCCATAATTCGAATGAATGTCAGT 1081  
Db 1875 TGTCAAGCGCTGTGAGGAAATTTGTCCCTGTTGTCTCCATAATTCGAATGAATGTCAGT 1934  
QY 1082 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAGTCTG 1141  
Db 1935 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAGTCTG 1994  
QY 1142 GAGTCAAGGATGTCATAGTCACTCACTGATGTGCTCTGGAACACCCAGGAAATGTG 1201  
Db 1995 GAGTCAAGGATGTCATAGTCACTCACTGATGTGCTCTGGAACACCCAGGAAATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAAACGCGAGGAGGTPAATGCGAGCCTTCGTAGCAGCACACGTGAG 1261  
Db 2055 ACTGTGTGTAGAGGAAACGCGAGGAGGTPAATGCGAGCCTTCGTAGCAGCACACGTGAG 2114  
QY 1262 CACTGCAATCTGTATACCCCAAGACACCTTCATCCCAAGGTTGGCGGAGG 1321  
Db 2115 CACTGCAATCTGTATACCCCAAGACACCTTCATCCCAAGGTTGGCGGAGG 2174  
QY 1322 CTCTCAGTCTGATGCTGCTATGTTAAAGATCTTACTGCTCCAAACCAAAATTCAG 1381  
Db 2175 CTCTCAGTCTGATGCTGCTATGTTAAAGATCTTACTGCTCCAAACCAAAATTCAG 2234  
QY 1382 TTGTTTGTCTCAATAGCCTTCCCTGAGGACTTCAAGTGTCTTTTAAAGACAGAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCCTTCCCTGAGGACTTCAAGTGTCTTTTAAAGACAGAGGC 2294  
QY 1442 ACCAAGAGGATCAATCACAAGCACTGC 1470  
Db 2295 ACCAAGAGGATCAATCACAAGCACTGC 2323

RESULT 4  
AAD04650  
ID AAD04650 standard; DNA; 3571 BP.

XX AAD04650;  
XX AC  
XX DT 04-JUL-2001 (first entry)  
XX DE Mouse Zveg3f3 DNA.  
XX KW Mouse; Zveg3f3 antagonist; cell proliferation; stellate cell activation;  
KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;  
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;  
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;  
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;  
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;  
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;  
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;  
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;  
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;  
KW fibroproliferative disorder; ds.  
XX OS Mus musculus.  
XX FH Key Location/Qualifiers  
FT CDS 1049..2086  
FT /tag= a  
FT /product= "Mouse Zveg3f3 protein"  
XX WO200128586-A1.  
XX PD 26-APR-2001.  
XX XX 23-OCT-2000; 2000WO-US29270.  
XX PF 21-OCT-1999; 99US-0161653.  
XX PR 12-NOV-1999; 99US-0165255.  
XX PR 01-AUG-2000; 2000US-0222223.  
XX XX (ZYMO ) ZYMOGENETICS INC.  
XX XX Gilbertson DG;  
XX PI WPI; 2001-300278/31.  
XX XX P-PSDB; AAE00998.  
XX DR Use of zveg3f3 antagonist for reducing fibroproliferative disorder of  
XX PT kidney, liver and bone, reducing extracellular matrix production,  
XX PT treating fibrosis or reducing stellate cell activation in mammal  
XX PS Example 2; Page 58-61; 70pp; English.  
XX CC The patent discloses materials and methods for reducing cell  
CC proliferation or extracellular matrix production, treating fibrosis and  
CC reducing stellate cell activation in a mammal. The method comprises  
CC administering a composition containing a Zveg3f3 antagonist in combination  
CC with a delivery vehicle. The Zveg3f3 is a protein that is structurally  
CC related to platelet-derived growth factor (PDGF) and the vascular  
CC endothelial growth factors (VEGF). The Zveg3f3 protein is also designated  
CC as "VEGF-R" and "PDGF-C". The Zveg3f3 antagonist is useful to block the  
CC mitogenic effects of zveg3f3 and thereby to inhibit or prevent and treat  
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active  
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and  
CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as  
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic  
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders  
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,  
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,  
CC fibrotic disorders of pancreas, fibroproliferative disorders of the  
CC vasculature such as transplant vasculopathy and hyperostosis.  
CC Disorders of the bone such as osteopetrosis and hyperostosis.  
XX CC The present sequence is mouse Zveg3f3 DNA.  
SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match

98.0%; Score 1444.8; DB 22; Length 3571;

Best Local Similarity 99.4%; Pred. No. 0;				
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;				
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGGAAAATTTTGGATGGGATATATGTGGAACCTA	61	
Db	856	AACTGGAGACACAGAGAGGGCTCTAGGAAAATTTTGGATGGGATATATGTGGAACCTA	915	
QY	62	CCCTGGGATTTCTCTGCTGCAGAGCGGCCGCTCCACCGCAGCGACGCCCTTTCC	121	
Db	916	CCCTGGGATTTCTCTGCTGCAGAGCGGCCGCTCCACCGCAGCGACGCCCTTTCC	975	
QY	122	CGGGCTGGGCTGAGCCCTTGGAGTCGTCCTTCCAGTCCCGCCGCGAGTGAGCCCTCG	181	
Db	976	C-GGCTGGGCTGAGCCCTTGGAGTCGTCCTTCCAGTCCCGCCGCGAGTGAGCCCTCG	1034	
QY	182	CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCC	241	
Db	1035	CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCC	1094	
QY	242	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGCGACA	301	
Db	1095	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGCGACA	1154	
QY	302	AGGAAACAGAACCGAGTGCAGATCCCGGCATGAGAGAGTTGTCATATATCTGTGAATG	361	
Db	1155	AGGAAACAGAACCGAGTGCAGATCCCGGCATGAGAGAGTTGTCATATATCTGTGAATG	1214	
QY	362	GGAGCATCCACAGCCGAGTTTCCTCATACGTACCCAGCAATATGGTGGTGGGA	421	
Db	1215	GGAGCATCCACAGCCGAGTTTCCTCATACGTACCCAGCAATATGGTGGTGGGA	1274	
QY	422	GATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGGC	481	
Db	1275	GATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGGC	1334	
QY	482	TGGAAGATCCAGAACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG	541	
Db	1335	TGGAAGATCCAGAACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG	1394	
QY	542	ATGGAAGTGTTTTAGGACGCTGTGTGTTCTGGGACTGTGCCAGAAACGACACTTCTA	601	
Db	1395	ATGGAAGTGTTTTAGGACGCTGTGTGTTCTGGGACTGTGCCAGAAACGACACTTCTA	1454	
QY	602	AAGCAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT	661	
Db	1455	AAGCAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT	1514	
QY	662	TCTGCAATCCACTACGATATATCATGCCACAAGTACAGAAACCAAGTCCTTCGGTGT	721	
Db	1515	TCTGCAATCCACTACGATATATCATGCCACAAGTACAGAAACCAAGTCCTTCGGTGT	1574	
QY	722	TGCCCCCTTCATCTTTGTCAATGGACCTGCTCAACATGCTGTGACTGCCCTTCAGTACCT	781	
Db	1575	TGCCCCCTTCATCTTTGTCAATGGACCTGCTCAACATGCTGTGACTGCCCTTCAGTACCT	1634	
QY	782	TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAATTCGACGCTCT	841	
Db	1635	TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAATTCGACGCTCT	1694	
QY	842	ACAAGCCACAATGGCAGCTTTTGGGCAAGCTTTCTCTGTATGGGAAAAGCAAGTGG	901	
Db	1695	ACAAGCCACAATGGCAGCTTTTGGGCAAGCTTTCTCTGTATGGGAAAAGCAAGTGG	1754	
QY	902	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTTACAGTGCACACCCCGGAATCTCT	961	
Db	1755	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTTACAGTGCACACCCCGGAATCTCT	1814	
QY	962	CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGTCTCC	1021	
Db	1815	CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGTCTCC	1874	
QY	1022	TGGTCAAGCGCTGTGGAGGAAATGTGCTGTGTTCTTCCATATTTGCAATGATGTAGT	1081	
Db	1875	TGTCACAGCGCTGTGGAGGAAATTTGCTGTGTTCTTCCATATTTGCAATGATGTAGT	1934	
QY	1082	GTGTCACCGCTGTAAAGCTTACAAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAACTG	1141	
Db	1935	GTGTCACCGCTGTAAAGCTTACAAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAACTG	1994	
QY	1142	GAGTCAAGGGATTTGCATAGTCACTCATGTGTGGCTCTGGAAACACCCAGGAGATGTG	1201	
Db	1995	GAGTCAAGGGATTTGCATAGTCACTCATGTGTGGCTCTGGAAACACCCAGGAGATGTG	2054	
QY	1202	ACTGTGTGTGTAGAGAAACGAGGAGGTAACTGCAGCTTCTGTAGCAGCACACCTGAG	1261	
Db	2055	ACTGTGTGTGTAGAGAAACGAGGAGGTAACTGCAGCTTCTGTAGCAGCACACCTGAG	2114	
QY	1262	CACCTGGCATTTCTGTGTACCCCCCAAGCAACCTTATCCCCACAGCGTTGGCCGAGGG	1321	
Db	2115	CACCTGGCATTTCTGTGTACCCCCCAAGCAACCTTATCCCCACAGCGTTGGCCGAGGG	2174	
QY	1322	CTCTCAGCTGT	1381	
Db	2175	CTCTCAGCTGT	2234	
QY	1382	TTGTTTGTCTTCAATAGCCCTTCCCTGCGAGCTTCAAGTGTCTTCTAAAGACCCAGAGC	1441	
Db	2235	TTGTTTGTCTTCAATAGCCCTTCCCTGCGAGCTTCAAGTGTCTTCTAAAGACCCAGAGC	2294	
QY	1442	ACCAAGAGGAGTCAATCAACAAAGCACTGC	1470	
Db	2295	ACCAAGAGGAGTCAATCAACAAAGCACTGC	2323	
RESULT 5				
ABS68648				
ID	ABS68648 standard; cDNA; 3571 BP.			
AC	ABS68648;			
XX	19-NOV-2002 (first entry)			
DT	Mouse cDNA encoding VEGF-like protein zveg1 3.			
DE	ss; gene; VEGF; vascular endothelial growth factor; zveg1 3;			
XX	chromosome 3; cell proliferation; differentiation; metabolism;			
KW	migration; revascularisation; solid tumour; diabetic retinopathy;			
KW	psoriasis; rheumatoid arthritis; cancer; autoimmune disease;			
KW	inflammation; myocardial ischaemia; scleroderma; fibrosis; mouse;			
KW	glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;			
KW	skin grafting; female reproductive tract disorder; chronic liver disease;			
KW	circulatory disorder; heart failure; neurodegenerative disease;			
KW	multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;			
KW	neurite outgrowth.			
OS	Mus musculus.			
XX	US6432673-B1.			
XX	13-AUG-2002.			
XX	07-DEC-1999; 99US-0457066.			
XX	07-DEC-1998; 98US-111173P.			
PR	06-JUL-1999; 99US-142576P.			
PR	21-OCT-1999; 99US-161653P.			
PR	12-NOV-1999; 99US-165255P.			
XX	(ZYMO) ZYMOGENETICS INC.			
XX	Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KB;			
PI	Gilbertson DG, West JW;			
XX	WPI; 2002-689759/74.			
DR	P-PSDB; ABG92894.			
XX				

PT Novel polypeptide, designated zvegf3 useful for treating skin wounds,  
PT ulcers, burns, skin grafting, female reproductive tract disorders,  
PT Parkinson's disease, and Alzheimer's disease -  
XX  
XX Example 4; Column 97-104; 68pp; English.

CC The invention relates to an isolated polypeptide, designated zvegf3  
CC (a vascular endothelial growth factor-like protein) of 111-136 amino acid  
CC residues in length and comprises the sequence appearing as ABG92889  
CC from amino acid residues 235-345. Also included are an isolated  
CC protein comprising a first polypeptide disulphide bonded to a second  
CC polypeptide, where each of the first and second polypeptides is from  
CC zvegf 3, and where the protein modulates cell proliferation,  
CC differentiation, metabolism or migration, the zvegf 3 encoding  
CC polynucleotides and zvegf 3 expression vectors and host cells.  
CC Zvegf 3 is useful as additives in tissue adhesives for promoting  
CC revascularisation of the healing tissue, for designing molecules that  
CC antagonise semaphorin-stimulated activities, including neurite growth,  
CC cardiovascular development, cartilage and limb development, and T and  
CC B-cell function, and for imaging tumours or other sites of abnormal cell  
CC proliferation and in gene therapy applications. The proteins are useful  
CC therapeutically to stimulate tissue development or repair, or cellular  
CC differentiation or proliferation, for stimulating the growth of  
CC fibroblast or smooth muscle cells, as molecular weight standards, as  
CC reagents in assays for determining circulatory level of the protein or as  
CC standards in the analysis of cell phenotype, for identifying inhibitors  
CC of their activity which are useful for reducing the growth of solid  
CC tumours, for treating diabetic retinopathy, psoriasis, rheumatoid  
CC arthritis, various forms of cancers, autoimmune disease, inflammation,  
CC myocardial ischaemia, scleroderma, and reducing fibrosis, including scar  
CC formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis,  
CC asbestosis), kidney fibrosis (including diabetic nephropathy),  
CC glomerulosclerosis, atherosclerosis, skin wounds, ulcers, burns, skin  
CC grafting, and female reproductive tract disorders, chronic liver disease  
CC (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory  
CC disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac  
CC sclerosis, neurodegenerative diseases such as multiple sclerosis,  
CC Parkinson's disease, Alzheimer's disease, and for regenerating neurite  
CC outgrowths following strokes. The gene for mouse zvegf3 is located on  
CC chromosome 3. The present sequence encodes zvegf 3.

XX  
SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match 98.0%; Score 1444.8; DB 24; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
2 ACCTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTTATGTGAAACTA 61  
856 AACTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTTATGTGAAACTA 915  
62 CCCTGGATTTCTGTGCGCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCTTTCCC 121  
916 CCCTGGCATTTCTGTGTCGACAGCGCGCGAGGCGCTTCCACCGCAGCGAGCTTTCCC 975  
122 CGGCGTGGCGCTGAGCTTTGGAGTGTGCTTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 181  
976 C-GGCTGGCTGAGCTTTGGAGTGTGCTTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 1034  
182 CCCAGTCAGCCAAATGTCTCTCTGCGGCTCTCTCTGCTGACATCTGCTGCGCGGCC 241  
1035 CCCAGTCAGCCAAATGTCTCTCTGCGGCTCTCTCTGCTGACATCTGCTGCGCGGCC 1094  
242 AAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 301  
1095 AAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 1154  
302 AGGAACAGACCGAGTGAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 361  
1155 AGGAACAGACCGAGTGAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214  
362 GGAGCATCCACAGCCCGAAGTTTCTCTATACGTACCCAGAAATATGGTGTGTGTGGA 421

Db 1215 GGAGCATCCACAGCCCGAAGTTTCTCTCATACATACCAAGAAATATGGTGTGTGGA 1274  
Qy 422 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
Db 1275 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334  
Qy 482 TGGAAATCCAGAAAGCATATATCAAGTATGATTTCTAGAAATTTGAGAGCCCAAGTG 541  
Db 1335 TGGAAATCCAGAAAGCATATATCAAGTATGATTTCTAGAAATTTGAGAGCCCAAGTG 1394  
Qy 542 ATGGAAGTGTTTTGGAGCGCTGTGTGGTCTCGGACTGTGCCAGGAAAGACAGACTTCTA 601  
Db 1395 ATGGAAGTGTTTTGGAGCGCTGTGTGGTCTCGGACTGTGCCAGGAAAGACAGACTTCTA 1454  
Qy 602 AAGGAAATCATATCAGGATAAAGATTTGTATCTCATGAGTATTTTCAATCTGAACCCCGAT 661  
Db 1455 AAGGAAATCATATCAGGATAAAGATTTGTATCTCATGAGTATTTTCCATCTGAACCCCGAT 1514  
Qy 662 TCTGCATCCACTACAGTATTTATCATGCCACAAGTCAAGAAACACAGAGTCCCTTCGGTGT 721  
Db 1515 TCTGCATCCACTACAGTATTTATCATGCCACAAGTCAAGAAACACAGAGTCCCTTCGGTGT 1574  
Qy 722 TSCCCCTTTCATCTTGTGCTGAGCTGCTCAACATGCTGTGACTGCCCTTCAGTACCT 781  
Db 1575 TSCCCCTTTCATCTTGTGCTGAGCTGCTCAACATGCTGTGACTGCCCTTCAGTACCT 1634  
Qy 782 TGGAAAGTGTATTCGGTACCTAGAGCCAGATGATGGAGGTGAGCTTGAGACGCTCT 841  
Db 1635 TGGAAAGTGTATTCGGTACCTAGAGCCAGATGATGGAGGTGAGCTTGAGACGCTCT 1694  
Qy 842 ACAAGCCAAATGCGCAGCTTTTGGGCAAGCTTTTCCGTATGGGAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAAATGCGCAGCTTTTGGGCAAGCTTTTCCGTATGGGAAAAAGCAAGTGG 1754  
Qy 902 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGGAATCTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGGAATCTCT 1814  
Qy 962 CAGTGTCCATACCGGAAAGAGCTAAAGAGGACAGATACCATATTTGGCCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCCATACCGGAAAGAGCTAAAGAGGACAGATACCATATTTGGCCAGGTTGTCTCC 1874  
Qy 1022 TGGTCAAGCGCTGTGGAGGAAATTTGCGCTGTTCTCTCCATATTTGCAATGCAATCTCAGT 1081  
Db 1875 TGGTCAAGCGCTGTGGAGGAAATTTGCGCTGTTCTCTCCATATTTGCAATGCAATCTCAGT 1934  
Qy 1082 GTGTCCACAGTAAAGTTTACAAAAAGTACCAATGAGTCTTTCAGTTGAGACCAAAACTG 1141  
Db 1935 GTGTCCACAGTAAAGTTTACAAAAAGTACCAATGAGTCTTTCAGTTGAGACCAAAACTG 1994  
Qy 1142 GAGTCAAGGGATTCATAAGTCACTCACTGATGTGGCTCTGGAAACACACAGGAAATGTG 1201  
Db 1995 GAGTCAAGGGATTCATAAGTCACTCACTGATGTGGCTCTGGAAACACACAGGAAATGTG 2054  
Qy 1202 ACTGTGTGTAGAGGAAACGAGGGTAACTGACGCTTTCGAGCAGTCTGAGCAGCAGTCA 1261  
Db 2055 ACTGTGTGTAGAGGAAACGAGGGTAACTGACGCTTTCGAGCAGTCTGAGCAGCAGTCA 2114  
Qy 1262 CACTGGCATTCGTGTATCCCCCAAGCAACCTTCATCCCCACAGCGTGTGGCCCGCAGGG 1321  
Db 2115 CACTGGCATTCGTGTATCCCCCAAGCAACCTTCATCCCCACAGCGTGTGGCCCGCAGGG 2174  
Qy 1322 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 1381  
Db 2175 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 2234  
Qy 1382 TTGTTTGTCTCAATAGCCTTCCCTGACGAGCTTCAAGTGTCTTCTTAAAGACCAAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCCTTCCCTGACGAGCTTCAAGTGTCTTCTTAAAGACCAAGGC 2294  
Qy 1442 ACCAAGAGGAGTCAATCAAAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCAAAAGCACTGC 2323

RESULT 6  
AAI72444  
ID AAI72444 standard; cDNA; 3571 BP.  
XX  
AC AAI72444;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Mouse zveg3 coding sequence.  
XX  
KW Gene; human; mouse; zveg3; zveg4; platelet derived growth factor;  
PDGF; homolog; growth; bone; ligament; cartilage; proliferation;  
osteoblast; chondrocyte; bony defect; fracture; bone graft;  
implant; periodontal pocket; osteoclast; bone marrow stem cell;  
osteoporosis; ss.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
CDS 1049..2086  
FT /\*tag= a  
FT /product= "zveg3"  
XX  
FN US200204225-A1.  
XX  
PD 10-JAN-2002.  
XX  
XX 29-MAR-2001; 2001US-0823033.  
XX  
PR 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142578P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
PR 31-MAR-2000; 2000US-193723P.  
PR 07-DEC-1999; 99US-0457066.  
XX  
XX (HART/) HART C E.  
XX (GILB/) GILBERTSON D G.  
XX  
XX Hart CE, Gilbertson DG;  
XX  
XX WPI; 2002-171026/22.  
XX P-PSDB; AAB47890.  
XX  
XX Promoting growth of bone, ligament or cartilage in a mammal, involves  
administering to the mammal a protein which comprises growth factor  
domain of zveg3 protein, a homolog of platelet-derived growth factor  
-  
XX  
XX Disclosure; Page 16-19; 31pp; English.  
XX  
XX The sequences given in AAI72443-44 encode human and mouse zveg3,  
respectively. zveg3 is a platelet derived growth factor (PDGF) homolog  
and it was used in the method of the invention for promoting growth of  
bone, ligament or cartilage and stimulating proliferation of osteoblasts  
or chondrocytes in a mammal. The proteins used were preferably a dimeric  
protein of residues 235-345 of human zveg3 or all of the mouse zveg3  
protein, with a delivery vehicle. The method of the invention is useful  
for promoting growth of bone, ligament or cartilage in a mammal, where  
the composition is administered at a site of a bony defect, preferably  
a fracture, bone graft site, implant site, or periodontal pocket, and  
for stimulating proliferation of osteoblasts or chondrocytes in a  
mammal. It is further useful for promoting proliferation of osteoblasts,  
osteoclasts, chondrocytes or bone marrow stem cells, where the bone  
marrow stem cells are harvested from a patient prior to culture. The  
method is therefore useful for treating osteoporosis.  
XX  
XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;  
SQ

Query Match 98.0%; Score 1444.8; DB 24; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;

	Matches	1460;	Conservative	0;	Mismatches	8;	Indels	1;	Gaps	1;
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGAACTA	61							
DB	856	AACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGAACTA	915							
QY	62	CCCTGGATTCTCTGCTGCAGAGCGCGCGCTTCCACCGAGCGGAGCTTCCC	121							
DB	916	CCCTGGATTCTCTGCTGCAGAGCGCGCGCTTCCACCGAGCGGAGCTTCCC	975							
QY	122	CGGGCTGGGCTGAGCCTTGGAGTCGCTCCCAAGTGCCTCCCGAGTGCCTCCG	181							
DB	976	C-GGCTGGGCTGAGCCTTGGAGTCGCTCCCAAGTGCCTCCCGAGTGCCTCCG	1034							
QY	182	CCCACTGCAGCCAAATGCTCCTCTCGGCCCTCTCTGTGATCATCTGCGCCGCC	241							
DB	1035	CCCACTGCAGCCAAATGCTCCTCTCGGCCCTCTCTGTGATCATCTGCGCCGCC	1094							
QY	242	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA	301							
DB	1095	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA	1154							
QY	302	AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGTGTGTCACTATATCTGTAATG	361							
DB	1155	AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGTGTGTCACTATATCTGTAATG	1214							
QY	362	GGAGCATCCACAGCCCGAAGTTTCTCTCATAGTACCAAGAAATATGGTGTGTGGGA	421							
DB	1215	GGAGCATCCACAGCCCGAAGTTTCTCTCATAGTACCAAGAAATATGGTGTGTGGGA	1274							
QY	422	GATTAGTTGAGTAGATGAAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC	481							
DB	1275	GATTAGTTGAGTAGATGAAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC	1334							
QY	482	TGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGAGCGCCAGTG	541							
DB	1335	TGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGAGCGCCAGTG	1394							
QY	542	ATGGAAGTGTTTTAGGACGCTGGTGTGGACTGTGCCAGAGAAAGAGACTTCTA	601							
DB	1395	ATGGAAGTGTTTTAGGACGCTGGTGTGGACTGTGCCAGAGAAAGAGACTTCTA	1454							
QY	602	AAGAAATCATATCAGGATAGATTTGATCTGATGATATTTTCCATCTGACCCGGAT	661							
DB	1455	AAGAAATCATATCAGGATAGATTTGATCTGATGATATTTTCCATCTGACCCGGAT	1514							
QY	662	TCTGCATCCACTACAGTATTATATGACCAAGTCCAGAAACACAGAGTCTTCCGTTGT	721							
DB	1515	TCTGCATCCACTACAGTATTATATGACCAAGTCCAGAAACACAGAGTCTTCCGTTGT	1574							
QY	722	TGCCCCCTTCATCTTTTGTTCATTTGGACCTGCTCAACAATGCTGAGTCTGCTTACCT	781							
DB	1575	TGCCCCCTTCATCTTTTGTTCATTTGGACCTGCTCAACAATGCTGAGTCTGCTTACCT	1634							
QY	782	TGGAGAGCTGATTCGTTACCTAGGCGAGATCCAGTGCAGTGTGAGTCTTGGACAGCTCT	841							
DB	1635	TGGAGAGCTGATTCGTTACCTAGGCGAGATCCAGTGCAGTGTGAGTCTTGGACAGCTCT	1694							
QY	842	ACAAGCCAACTAGGAGCTTTTGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAGTGG	901							
DB	1695	ACAAGCCAACTAGGAGCTTTTGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAGTGG	1754							
QY	902	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTACAGCTGCGACACCCCGGAATCTT	961							
DB	1755	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTACAGCTGCGACACCCCGGAATCTT	1814							
QY	962	CACTGTCCATACGGAAGAGCTTAAGAGGACAGATACCATATCTTGGCCAGGTGTCTCC	1021							
DB	1815	CAGTGTCCATACGGAAGAGCTTAAGAGGACAGATACCATATCTTGGCCAGGTGTCTCC	1874							
QY	1022	TGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTTGTCTCCATTAATGCAATGATGTCA	1081							
DB	1875	TGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTTGTCTCCATTAATGCAATGATGTCA	1934							

QY 1082 GTGTCACGTAAGTTACAAAAGTACCAATGAGTCCCTTCACTGAGACCAAACTG 1141  
|  
|  
|  
Db 1935 GTGTCACGTAAGTTACAAAAGTACCAATGAGTCCCTTCACTGAGACCAAACTG 1994  
|  
|  
|  
QY 1142 GAGTCAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACCCAGGAAATGTG 1201  
|  
|  
|  
Db 1995 GAGTCAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACCCAGGAAATGTG 2054  
|  
|  
|  
QY 1202 ACTGTGTGTAGAGAAACGAGAGGGTAACTGACGCTTCTGAGCAGCACAGTGAG 1261  
|  
|  
|  
Db 2055 ACTGTGTGTAGAGAAACGAGAGGGTAACTGACGCTTCTGAGCAGCACAGTGAG 2114  
|  
|  
|  
QY 1262 CACTGGCAATCTGTGTACCCCAAGCAACTCTCATCCCAACGAGCTTGGCCGACGG 1321  
|  
|  
|  
Db 2115 CACTGGCAATCTGTGTACCCCAAGCAACTCTCATCCCAACGAGCTTGGCCGACGG 2174  
|  
|  
|  
QY 1322 CTCTCAGCTGTGTGTGGCTGTATGTTAAAGATCTTACTCTCAACCAAAATCTCAG 1381  
|  
|  
|  
Db 2175 CTCTCAGCTGTGTGTGGCTGTATGTTAAAGATCTTACTCTCAACCAAAATCTCAG 2234  
|  
|  
|  
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGACGACTTCAAGTGTCTTAAAGACCAAGGC 1441  
|  
|  
|  
Db 2235 TTGTTTGTCTCAATAGCTTCCCTGACGACTTCAAGTGTCTTAAAGACCAAGGC 2294  
|  
|  
|  
QY 1442 ACCAAGAGTCAATCAAGCACTGC 1470  
|  
|  
|  
Db 2295 ACCAAGAGTCAATCAAGCACTGC 2323  
|  
|  
|

RESULT 7

ABX93182  
ID ABX93182 standard; DNA; 3571 BP.

XX AC  
XX ABX93182;

DT 22-MAY-2003 (first entry)

XX DNA encoding mouse growth factor homologue, zvegfg3.

XX Mouse; growth factor homologue; zvegfg3; fibroblast; smooth muscle cell;  
KW cell-surface platelet-derived growth factor alpha receptor; PDGF;  
KW full-thickness skin wound; female reproductive tract; duodenal ulcer;  
KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;  
KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;  
KW chronic active hepatitis; hepatic chronic passive congestion; stroke;  
KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;  
KW portal vein thrombosis; cardiac sclerosis; new vessel formation;  
KW endothelial precursor stem cell; neovascularisation; wound healing;  
KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;  
KW sensory neurite outgrowth; brain damage; head injury; paralysis;  
KW spinal injury; neurodegenerative disease; diabetic retinopathy;  
KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;  
KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;  
KW proliferative vascular disorder; ocular neovascularisation;  
KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;  
KW angiogenesis; nervous system disorder; cytostatic; hepatotropic;  
KW vulvar; tranquilliser; cerebroprotective; neuroprotective; nootropic;  
KW ophthalmological; dermatological; coagulant; cardiant; chromosome 3;  
gene; ds.

XX Mus musculus.

XX Key Location/Qualifiers  
FH 1049..2086  
CDS /\*tag= a  
FT /product= "Zvegfg3"  
FT

XX US2002177193-A1.

XX 28-NOV-2002.

XX 02-MAY-2002; 2002US-0139583.

XX 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142576P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
PR 07-DEC-1999; 99US-0457066.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KB;  
PI Gilbertson DG, West JW;  
XX  
XX WPI; 2003-328485/31.  
DR P-PSDB; ABG76398.  
XX  
XX New isolated zvegfg3 polypeptide, useful for treating cancer,  
PT Alzheimer's disease, Parkinson's disease, chronic active hepatitis,  
PT hepatic vein thrombosis, comprises growth factor domain and CUB domain  
PT .  
XX  
XX Example 4; Page 53-55; 73pp; English.

XX The present invention relates to the isolation of a growth factor  
CC homologue referred to as zvegfg3, and the polynucleotide sequence  
CC encoding it. The zvegfg3 polypeptide is useful for stimulating the  
CC growth of fibroblasts or smooth muscle cells, or for activating a  
CC cell-surface platelet-derived growth factor (PDGF) alpha receptor.  
CC The zvegfg3 polypeptide is useful as a PDGF alpha receptor agonist and  
CC thus is useful for treating full-thickness skin wounds, female  
CC reproductive tract and prolonged bleeding, periodontal disease,  
CC damaged liver tissue, and duodenal ulcers. The polypeptide is also  
CC useful as an additive in tissue adhesives for promoting  
CC revascularisation of healing tissue. The zvegfg3 polypeptide is also  
CC useful for treating liver damage including damage due to liver  
CC disease, chronic active hepatitis, hepatic chronic passive congestion  
CC (CPC), central haemorrhagic necrosis (CHN), hepatic vein thrombosis,  
CC portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis.  
CC The polypeptide is useful for enhancing expansion and mobilisation of  
CC endothelial precursor stem cells, creating and stabilising new vessel  
CC formation in areas requiring neovascularisation, including areas of  
CC ischaemia, organ transplants, wound healing, and tissue grafting. It  
CC may be used for treating peripheral neuropathies by increasing spinal  
CC cord and sensory neurite outgrowth, and as part of therapeutic  
CC treatment for the regeneration of neurite outgrowths following strokes,  
CC brain damage caused by head injuries, and paralysis caused by spinal  
CC injuries. Application may also be made in treating neurodegenerative  
CC diseases (e.g. multiple sclerosis, Alzheimer's disease, Parkinson's  
CC disease), diabetic retinopathy, psoriasis, arthritis, scleroderma, and  
CC reducing fibrosis, keloids, liver fibrosis, lung fibrosis, kidney  
CC fibrosis, and glomerulosclerosis. An antibody that binds zvegfg3 is  
CC useful for blocking the mitogenic, chemotactic, or angiogenic effects  
CC of zvegfg3, and for treating proliferative vascular disorders, ocular  
CC neovascularisation, inflammatory disorders, rheumatoid arthritis,  
CC psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,  
CC and diseases of the nervous system. The present sequence encodes  
CC mouse zvegfg3. The gene encoding mouse zvegfg3 maps to chromosome 3.

XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

XX Query Match 98.0%; Score 1444.8; DB 25; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
|  
|  
|  
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915  
|  
|  
|  
QY 62 CCCTGCGAATTCCTGTGCGCAGAGCCGCGCGGCTTCCACCCGAGCGAGCTTTCCC 121  
|  
|  
|  
Db 916 CCCTGCGAATTCCTGTGCGCAGAGCCGCGCGGCTTCCACCCGAGCGAGCTTTCCC 975  
|  
|  
|  
QY 122 CGGGCTGGCTGAGCCTTGAGTGTGCTCTCCCACTCCCGCGGCGAGTGAGCCTTCG 181  
|  
|  
|





CC skin graft growth, tissue repair, proliferation of new blood vessels,  
CC tissue regeneration and organ repair by promoting angiogenic activity or  
CC vascularization. This sequence encodes the human VEGF-X protein isolated  
CC from clones 4 and 7 described in the method of the invention.  
XX  
SQ Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;

Query Match 62.0%; Score 914.2; DB 21; Length 1473;  
Best Local Similarity 83.5%; Pred. No. 11e-267;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGCGCTCTAGGAAATAATTTGGATGGGATATATGTGAAACTA 61  
DB 59 AACTGGAGACACAGAGAGCGCTCTAGGAAATAATTTGGATGGGATATATGTGAAACTA 118  
QY 62 CCTCGGATCTCTGCTGCAGAGCCGCGCAGCGCTTCCACCGCAGCGAGCTTCC 121  
DB 119 CCTCGGATCTCTGCTGCAGAGCGCGCTTCCACCGCAGCGAGCTTCC 178  
QY 122 CGG----GCTGGGCTGAGCCTTGAGTCTGCTTCCCGAGTCCCGCGAGTGAAGCC 177  
DB 179 TGGCGTGTGAAGACACTCGGAGTCTGCTTCCAAAGTCCCGCGTGAAGCT 238  
QY 178 CTGCCCCAGTCAAGCAATGCTCTCTCGGCTCTCTGCTGACATCTGCGCTGGCC 237  
DB 239 CTCACCCAGTCAAGCAATGAGCTCTTCGGGCTCTCTGCTGACATCTGCGCTGGCC 298  
QY 238 GGCCTGAAGACGGGAGCTCGGCTGAGTCCCACTGAGCAGTTCAGCTCTCCAGC 297  
DB 299 GGCCTGAAGACGGGAGCTCGGCTGAGTTCCACTGAGTGAATTCAGTTCCTCAGC 358  
QY 298 GACAAGGAACAGACGAGTGCAGATCCCGGATGAGAGAGTGTCACTATATCTGGT 357  
DB 359 AACAGGAACAGACGAGTGCAGATCCCTGAGTGAATTTACTGTCTACT 418  
QY 358 AATGGAGACATCAACAGCCGAGTTCCTCATACGTACCAAGAAATATGCTGCTGGTG 417  
DB 419 AATGGAGATTCACAGCCCAAGTTCCTCATATCTTATCCAGAAATACGCTCTGGTA 478  
QY 418 TGGAGATTTAGTTCAGTATGAAATGCGGATCCAGCTGACATTTGATGAGAGATTT 477  
DB 479 TGGAGATTTAGTTCAGTATGAAATGATGAGATACAACTTACGTTTGTGAAAGATTT 538  
QY 478 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAGTTGAGAGGCC 537  
DB 539 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAAGTTGAGAGGCC 598  
QY 538 AGTGATGGAAGTGTTTAGGACCGTGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACT 597  
DB 599 AGTGATGGAACATATATAGGCGCTGTGTGGTCTGGTACTGTACCAGGAAACAGATT 658  
QY 598 TCTAAGGAATCATATCAGGATGAAGTTTGTATGATGATTTTCCATCTGAAGCC 657  
DB 659 TCTAAGGAATCAATATGAGATGAAGTTTGTATGATGATTTTCCATCTGAAGCC 718  
QY 658 GGATTTCTGCATCCACTACAGTATATCATGCCACAGTACAGAAACACAGAGTCTTCG 717  
DB 719 GGGTTCTGCATCCACTACCAATTTGTATGATGATTTTCCATCTGAAGCC 778  
QY 718 GTGTGCCCCCTTCATCTTTGATGATGACCTGTCAACATGCTGTGACTGCTTCAAT 777  
DB 779 GTGTGCCCCCTTCAGCTTTGCACTGACCTGTCTTAATATGCTATTAATGCTTCAAT 838  
QY 778 ACCTTGGAAGAGCTGATTCGGTACCTAGAGCAGATCGATGCGAGTGCAGCTTGACAGC 837  
DB 839 ACCTTGGAAGACCTTATTCGATATCTTGAACAGAGATGCGATGCGATTTGAAGAT 898  
QY 838 CTCTACAGCCAAACATGCGAGCTTTTGGCAGAGCTTTCTGTATGGGAAATAAGCAAA 897  
DB 899 CTATATAGCCCACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGGAAATAATCCAGA 958  
QY 998 GTGTGGAATCTGAATCTCTCAAGGAAGGTAAACTCTCAGCTGCACACCCCGAAC 957

DB 959 GTGGTGAATCTGAACCTTTCTAAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1018  
QY 958 TTCTCAGTGTCCATACCGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGT 1017  
DB 1019 TTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCATATTTCTGGCCAGGTTGT 1078  
QY 1018 CTCTGCTCAAGCGCTGTGTGAGGAAATTTGTCCTGTTGTCTTCCATTAATTTGCAATGAATGT 1077  
DB 1079 CTCTGCTTAAAGCGCTGTGTGAGGAACTGTGCTCTGTTGTCTTCCCAATTTGCAATGAATGT 1138  
QY 1078 CAGTGTGTCCACGTAAGTTACAAAAAGTTACCATGAGTTCCTTCACTTGTGAGACCAAAA 1137  
DB 1139 CAATGTGTCTCCAGCAAGTTACTAAAAAATACCCAGGTCCTTCACTTGTGAGCAAAAG 1198  
QY 1138 ACTGGAGTCAAGGATTTCATAGTCACTCACTCATGTGGCTCTGGAAACACACGAGGAA 1197  
DB 1199 ACCGTTGTGAGGATTTCACAAATCACTCACGACGTGGCCCTGGAGCACCATTGAGGAG 1258  
QY 1198 TGTGACTGTGTGTGAGGAAACGAGGAGGTAACTGACGCTTGTGTAGCAGCAC 1254  
DB 1259 TGTGACTGTGTGTGAGGAGGAGCACAGGAGTAGCGCATCACCACGACGCTC 1315

RESULT 9  
ABQ81461  
ID ABQ81461 standard; cDNA; 2632 BP.  
XX  
AC ABQ81461;  
XX  
DT 19-DEC-2002 (first entry)  
XX  
DE Human vascular endothelial growth factor-X cDNA.  
XX  
KW Vascular endothelial growth factor-X; VEGF-X;  
KW platelet-derived growth factor-C; PDGF-C; human; smooth muscle;  
KW cell proliferation; tissue repair; antiarteriosclerotic; vulnerary;  
KW vasotrophic; uropathic; Gene therapy; chromosome 4q31-q32; gene; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 257..1294  
FT /tag= a  
FT /product= "VEGF-X"  
FT sig\_peptide 257..322  
FT /tag= b  
FT mat\_peptide 323..1291  
FT /tag= c  
FT misc\_feature 363..364  
FT /tag= d  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 568..569  
FT /tag= e  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 703..704  
FT /tag= f  
FT /note= "cryptic splice donor/acceptor site"  
FT misc\_feature 744..745  
FT /tag= g  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 942..943  
FT /tag= h  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 979..980  
FT /tag= i  
FT /note= "cryptic splice donor/acceptor site"  
FT misc\_feature 1165..1166  
FT /tag= j  
FT /note= "location of predicted mRNA splicing event"  
XX  
PN WO200272127-A2.  
XX  
PD 19-SEP-2002.



XX PF 07-MAR-2002; 2002WO-EP02616.  
XX PR 09-MAR-2001; 2001US-274901P.  
XX PA (JANC ) JANSSEN PHARM NV.  
XX PI Geesin JC, Gosiewska A, Xu J, Gordon R, Yon J, Dhanraj SN;  
XX PI Harris I;  
XX DR MPI: 2002-723297/78.  
XX DR P-PSDB; ABB79984.  
XX PT Use of vascular endothelial growth factor polypeptides, its CUB domain  
XX PT and polynucleotides, for manufacturing a medicament for treating or  
XX PT preventing diseases associated with reduced smooth muscle cell  
XX PT proliferation -  
XX PS Claim 1; Fig 1(a); 48pp; English.  
XX CC The present sequence is the cDNA sequence of human vascular  
XX CC endothelial growth factor-X (VEGF-X), or platelet-derived growth  
XX CC factor-C (PDGF-C), a novel member of the VEGF/PDGF family. The  
XX CC cDNA was obtained from a search of expressed sequence tag  
XX CC databases. Positions of mRNA splicing events were determined  
XX CC either from direct sequencing on an isolated BAC clone or by  
XX CC comparison of partial BAC database sequences. No information on  
XX CC splicing events is available for the region from nucleotides  
XX CC 900 to 957. Cryptic splice donor/acceptor sites were deduced from  
XX CC variant sequences isolated by PCR. The VEGF-X gene was localised  
XX CC to the long arm of human chromosome 4, region q31-q32. The VEGF-X  
XX CC protein, and its CUB domain, exhibit a mitogenic activity on human  
XX CC smooth muscle cell. Claimed methods of treating or preventing  
XX CC a urethral dysfunction, bladder dysfunction, pelvic floor  
XX CC reconstruction, sphincter dysfunction or a dysfunction associated  
XX CC with aberrant endogenous VEGF-X activity comprise administering a  
XX CC VEGF-X polypeptide (or its CUB domain), a nucleic acid molecule  
XX CC encoding it, an expression vector comprising the nucleic acid  
XX CC molecule, or a pharmaceutical composition comprising the nucleic  
XX CC acid molecule or polypeptide. Claimed methods of treating or  
XX CC preventing atherosclerosis, neointimal hyperplasia caused by artery  
XX CC anastomosis or balloon catheter, post-angioplasty restenosis  
XX CC caused by arterial stenting after percutaneous transluminal coronary  
XX CC angioplasty, comprise administering neutralising VEGF-X antibodies,  
XX CC antisense VEGF-X sequences or non-protein antagonists. Methods of  
XX CC diagnosing a pathological condition, or a susceptibility to such a  
XX CC condition, associated with smooth muscle cell proliferation, and  
XX CC for identifying compounds that inhibit or enhance smooth muscle  
XX CC cell proliferation, are also claimed.  
XX SQ Sequence 2632 BP; 772 A; 502 C; 557 G; 801 T; 0 other;  
  
Query Match 62.0%; Score 914.2; DB 24; Length 2632;  
Best Local Similarity 83.5%; Pred. No. 1.6e-267;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
  
Qy 2 ACCTGGAGACACAGAGGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 59 AACTGGAGACACAGAGGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 118  
  
Qy 62 CCCTGGGATTTCTGTGTCGACAGCGGCCAGGGCTTCCACCGCAGGCGAGCCTTCCC 121  
Db 119 CCCTGGGATTTCTGTGTCGACAGCGGCTCGGGGCTTCCACCCAGTGCAGCCTTCCC 178  
  
Qy 122 CGG---GCTGGGCTGAGCCTTGGATCGTCGCTTCCCGAGTGCAGGAGTGGCC 177  
Db 179 TGGCGGTGGTGAAGAAGACTCGGGAGTCGCTTCCAAAGTGGCCCGCGAGTGAGCT 238  
  
Qy 178 CTCGCCCCAGTCAGCAAAATGCTCTCTCGGCGCTTCTCTGCTGACATCTGCCCTGGCC 237  
Db 239 CTCACCCAGTCAGCCAAATGAGCTCTTTCGGGCTTCTCTGCTGACATCTGCCCTGGCC 298  
  
Qy 238 GGCCAAAGACGGGAGCTCGGGCTGAGTCCAAACCTGAGCAGCAAGTTGCACTCTCCAGC 297

Db 299 GGCCAGACAGGGGACTCAGGCGAATCCAACTGAGTAGTAAATTTCCAGTTTCCAGC 358  
Qy 298 GACAAGAAACAGAAACGAGTGCAGAGATCCCGCATGAGAGAGTGTGCACTATATCTGGT 357  
Db 359 AACAGAAACAGAAACGAGTGCAGAGATCCCGCATGAGAGAGTGTGCACTATATCTGGT 418  
Qy 358 AATGGGAGATCCACAGCCCGAAAGTTTCTCTATACGTAACCCAGAAATATGGTGCTGGT 417  
Db 419 AATGGAGATTTACAGCCCAAGTTTCTCTATACGTAACCCAGAAATATGGTGCTGGT 478  
Qy 418 TGGAGATTTAGTTCAGTAGATGAATGCGGATCCGATCCAGTGCATTTGATGAGAGATT 477  
Db 479 TGGAGATTTAGTTCAGTAGAGGAAATGTATGATACAACTTACGTTTGTATGAAGATT 538  
Qy 478 GGCTGGAAGATCCAGAAACGATATATGCAAGTATGATTTGTAGAAAGTTGAGGAGCCC 537  
Db 539 GGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAAAGTTGAGGAGCCC 598  
Qy 538 AGTATGGAGATGTTTTAGGACGCTGGTGTGGTCTTGGGACTGTGCCAGAAAGCAGACT 597  
Db 599 AGTATGGAGATATATTTAGGGGCTGGTGTGGTCTTGGTACTGTACCAGGAAACAGATT 658  
Qy 598 TCTAAAGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 659 TCTAAAGAAATCAATTAGGTAAGATTTGTATCTGATGAATATTTTCTTCTGAAACCA 718  
Qy 658 GGATTCGCATCCACTACAGTATTTATCATGCCCAAGTACAGAAACCAACAGTCTTTCG 717  
Db 719 GGGTTCGCATCCACTACACATTTGTCGCCCAATTTACAGAGCTGTGAGTCTTCA 778  
Qy 718 GTGTGCCCCCTTCATCTTTGTCAATGGAAGCTGCTCAACAAATGCTGTGACTGCCTCAGT 777  
Db 779 GTGTACCCCTTCAGCTTTGGCACTGCACTGCTTAATAATGCTATAACTGCTCTTAGT 838  
Qy 778 ACCTTGAAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGGTGGACTTGCACAGC 837  
Db 839 ACCTTGAAGAGCTTATTCGATATCTTGAACCCAGAGAGATGGCAGTTGGAATTAGAAGT 898  
Qy 838 CTCTACAAGCAACATCGCAGCTTTTGGCAAGGCTTTCTCTGTATGGGAAAAAAGCAAA 897  
Db 899 CTATATAGGCCAATCTTGGCAACTTCTTGGCAAGGCTTTGTTTGGAGAAATCCAGA 958  
Qy 898 GTGTGTAATCTGATCTCTCAAGAAAGAGTAAAACTCTACAGCTGCACACCCCGGAAC 957  
Db 959 GTGTGGATCTGAACCTTTAAACAGAGAGAGTAAAGATTATACAGCTGCACACCTCGTAAC 1018  
Qy 958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1017  
Db 1019 TTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCCGATACCATTTTCTGCCAGGTGT 1078  
Qy 1018 CTCTGCTCAAGCGCTGTGGAGAAATTTGCGCTTGTGTCTTCCATTAATTTGCAATGAATGT 1077  
Db 1079 CTCTGCTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCCCAATTTGCAATGAATGT 1138  
Qy 1078 CAGTGTGTCCACGTAAGTTTACAAAAAGTACCATGAGGTCCTTTCAGTTGAGACCAAAA 1137  
Db 1139 CAATGTGTCCCAAGCAAGTTTACTAAAAAATACACGAGGTCCTTTCAGTTGAGACCAAG 1198  
Qy 1138 ACTGAGTCAAGGATTTGCATTAAGTCACTCATGATGTGGCTCTGGACACACACAGGAA 1197  
Db 1199 ACCGGTGTGAGGATTTGCACAAATCACTCACCGAGTGGCCCTTGGACACCATGAGAG 1258  
Qy 1198 TGTGACTGTGTGTAGAGGAAACGCGAGGGGTAACTTGCAGCCTTCTGTAGCAGCAC 1254  
Db 1259 TGTGACTGTGTGTGACAGGGAGGACAGAGGAGTAGCGCATCACCCACAGCAGCTC 1315  
  
RESULT 10  
AAA71990  
ID AAA71990 standard; cDNA; 2668 BP.  
XX  
AC AAA71990;

```
XX XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX DT antiarthritis; antipsoriatic; antidiabetic; treatment;
XX DE Key CDS Location/Qualifiers
XX 19-JAN-2001 (first entry)
XX Human VEGF-X cDNA.
XX 267..1304
XX /*tag= a
XX /product= "VEGF-X"
XX WO200037641-A2.
XX 29-JUN-2000.
XX 21-DEC-1999; 99WO-US30503.
XX 22-DEC-1998; 98GB-0028377.
XX 18-MAR-1999; 99US-0124967.
XX 08-NOV-1999; 99US-0164131.
XX (JANC ) JANSSEN PHARM NV.
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
XX Dhanaraj SN, Xu J;
XX WPI: 2000-442669/38.
XX P-PSDB; AAB10844.
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis activity
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX Disclosure; Fig 30B; 127pp; English.
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
XX antidiabetic activity and acts as an angiogenesis and vascularization
XX regulator. An antisense molecule of the invention is useful for treating
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX retinopathy by inhibiting angiogenic activity or inappropriate
XX vascularization including formation and proliferation of new blood
XX vessels, growth and development of tissues, tissue regeneration and organ
XX and tissue repair in a subject. The products of the invention are useful
XX for preparing medicaments for treating wounds such as dermal ulcers,
XX pressure sores, venous sores, diabetic ulcers and burns and to promote
XX skin graft growth, tissue repair, proliferation of new blood vessels,
XX tissue regeneration and organ repair by promoting angiogenic activity or
XX vascularization. This sequence encodes a human VEGF-X protein described
XX in the method of the invention.
XX SQ Sequence 2668 BP; 780 A; 511 C; 567 G; 810 T; 0 other;
XX Query Match 62.0%; Score 914.2; DB 21; Length 2668;
XX Best Local Similarity 83.5%; Pred. No. 1.6e-267;
XX Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;
XX 2 ACCTGAGACACAGAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGTGGAACATA 61
XX 69 AACTGAGACACAGAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGTGGAACATA 128
XX 62 CCTCGGATTTCTGCTGCCAGAGCGGCCAGCGCTTCCACCGCAGCGAGCCTTTTCCC 121
XX 129 CCTCGGATTTCTGCTGCCAGAGCGGGCTCGCGGCTTCCACCGCAGCGAGCCTTTCCC 188
QY 122 CGG----GCTGGGCTGAGCCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCC 177
DB 189 TGGCGGTGGTGAAGAGAGACTCGGGAGTCTGCTTCCAAAGTCCCGCGCGTGAAGTACT 248
QY 178 CTCGCCCCAGTCAGCCAAATGCTCTCTCGGCGCTCTCTCTGTCACATCTGCTCCCTGGCC 237
DB 249 CTCACCCAGTCAGCCAAATGAGCTCTTTCGGGCTTCTCTGTCACATCTGCTCCCTGGCC 308
QY 238 GGCACAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAGGTTGAGCTCTCCAGC 297
DB 309 GGCACAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAATTTCCAGTTTCCAGC 368
QY 298 GACAAAGAACAGAACGGAGTCAAGATCCCGGCAATGAGAGAGTTGTCACTATATCTGTT 357
DB 369 AACAAAGAACAGAACGGAGTCAAGATCTCAGCATGAGAGAAATTAATCTGTCTACT 428
QY 358 AATGGAGCATCCACAGCGCCGAGTTTCTCATATGTCACCAAGAAATATGTTGCTGGTG 417
DB 429 AATGGAAGTATTCACAGCCCAAGTTTCTCATATCTTATCCAAAGAAATACGGTCTTGT 488
QY 418 TGGAGATTAGTTGACAGTAGATGAAATGTGCGGATCCAGCTGACATTTTGTATGAGATT 477
DB 489 TGGAGATTAGTAGCAGTAGAGGAAATGTATGATACAACTTACGTTTGTATGAAAGATT 548
QY 478 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 537
DB 549 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 608
QY 538 AGTGATGGAAGTGTGTTTAGGAGCTGTTGCTGCTGCTGCGACTGTGCCAGAAAGCAGACT 597
DB 609 AGTGATGGAACATATATTTAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
QY 598 TCTAAAGGAAATCATATCATGATTAAGATTGATCTGATGAGTATTTTCCATCTGAACCC 657
DB 669 TCTAAAGGAAATCAAATTAGGATAAGATTGATCTGATGAATATTTTCTCTGAAACCA 728
QY 658 GAATCTGATCCACTACAGTATATATGCAAGTATGATGCAAGTATGATGCAAGTATGAT 717
DB 729 GGGTTCTGATCCACTACAACTTGTATGCAAGTATGATGCAAGTATGATGCAAGTATG 788
QY 718 GTGTTGCCCTTCTATCTTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTC 777
DB 789 GTGCTACCCCTTCTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 848
QY 778 ACCTTGGAGAGCTGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
DB 849 ACCTTGGAGAGCTTATTCGATATCTTGAACAGAGAGATGCGAGTTGAGATTTAGA 908
QY 838 CTCTACAGCCCAACATGCGAGCTTTTGGGCAAGCTTTTCTGATGGGAAAAAGCAAA 897
DB 909 CTATATAGGCCAATTTGGCAACTTCTTGGCAAGCTTTTGTGTTTGGGAAAAATCCAGA 968
QY 898 GTGGTGAATCTCAATCTCTCTCAAGGAGAGGTAAAACTCTACAGCTGCAACCCCGAAC 957
DB 969 GTGGTGAATCTCAATCTCTCTCAAGGAGAGGTAAAGATTATACAGCTGCAACCTCG 1028
QY 958 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGAGACATACCATATTTGCGCCAGTTGT 1017
DB 1029 TTCTCAGTGTCCATTAAGGAGAGACTTAAAGAGAGACCATACCATTTTCTGCGCAG 1088
QY 1018 CTCCTGCTCAAGCGCTGTGGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077
DB 1089 CTCCTGTTTAAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1148
QY 1078 CAGTGTGCTCCAGTAAAGTACAAAAGTACCAATGAGTCCCTGCTGCTGCTGCTGCTGCT 1137
DB 1149 CAATGTGCTCCAGCAAGAGTGTACTAAAAATACCAAGAGTCTCTCAGTTGAGACCAAG 1208
QY 1138 ACTGAGTCAAGGAGTTGCAATAGTCACTCACTGATGCTGCTGCTGCTGCTGCTGCTGCT 1197
DB 1209 ACCGGTGTGAGGGGATTCACAAATCACTCACCGAGCTGGCCCTGGAGCAACCATGAGG 1268
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QY 1198 TGTGACTGTGTGTAGAGAAACGACGAGGAGTAACTGCACCTTCTGTAGCAGCAC 1254  
 |||||  
 DB 1269 TGTGACTGTGTGTAGAGGAGCAGAGGATAGCCGCTACACCACGACGCTC 1325  
 |||||

RESULT 11  
 AA23691  
 ID AA23691 standard; DNA; 2825 BP.  
 XX  
 AC AA23691;  
 XX 11-JAN-2000 (first entry)  
 XX Human VEGF-E DNA.  
 DE  
 XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
 XX treatment; cardiovascular disorder; endothelial disorder; therapy;  
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
 KW angiogenic disorder; age-related macular degeneration; vascular disease;  
 KW neovascularization; tumor; gene mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 259..1296  
 FT CDS /\*tag= a  
 FT /\*product= "VEGF-E"  
 XX  
 XX WO9947677-A2.  
 XX  
 XX 23-SEP-1999.  
 XX  
 XX 10-MAR-1999; 99WO-US05190.  
 XX  
 XX 17-MAR-1998; 98US-0040220.  
 XX 02-NOV-1998; 98US-0184216.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ferrara N, Kuo SS;  
 XX  
 XX WPI; 1999-580306/49.  
 DR P-PSDB; AAY33679.  
 XX  
 XX New growth factor polypeptide useful for treating cardiovascular or  
 PT endothelial disorders, e.g. cardiac hypertrophy  
 XX  
 XX Claim 2; Fig 1; 122pp; English.  
 XX  
 XX This invention describes the isolation of a novel human vascular  
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has  
 CC tranquilizer, vulny and cardiant activity. VEGF-E can be administered  
 CC therapeutically, especially by expressing encoding polynucleotides, to  
 CC treat cardiovascular or endothelial disorders in mammals, especially  
 CC humans. It is useful in wound repair and tissue generation and  
 CC regeneration, and may especially be used to treat cardiac hypertrophy  
 CC It can be combined with a carrier in pharmaceutical compositions, which  
 CC can be administered to treat disorders as above. VEGF-E can be used to  
 CC screen for antagonists and agonists, and the antagonists administered to  
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or  
 CC age-related macular degeneration. It can be used to generate antibodies,  
 CC useful therapeutically as antagonists, as above. The antibodies are also  
 CC useful to detect VEGF-E polypeptide, especially to diagnose  
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.  
 CC vascular disease, or neovascularization associated with tumor formation),  
 CC by contacting the antibody with a tissue sample and detecting formation  
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding  
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders  
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in  
 CC tissue samples. They can also be used to diagnose a disease or  
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a  
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by  
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a

CC sample. They may also be used to produce probes useful to detect related  
 CC sequences or for gene mapping. This sequence encodes the human VEGF-E  
 CC protein described in the method of the invention.  
 XX  
 SQ Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;  
 Query Match 62.0%; Score 914.2; DB 20; Length 2825;  
 Best Local Similarity 83.5%; Pred. No. 1.7e-267;  
 Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
 QY 2 ACCTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 61  
 |||||  
 DB 61 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 120  
 |||||  
 QY 62 CCCTGCGATTTCTCTGTCAGAGCGGCGCCAGCGCTTCCACCGCAGCGCAGCTTTTCCC 121  
 |||||  
 DB 121 CCCTGCGATTTCTCTGTCAGAGCGGCTCTGCGCTTCCACCGCAGCTTCCCTCCC 180  
 |||||  
 QY 122 CGG----GCTGGGCTGAGCCTTTGGAGTGTGCTCTCCCGAGTCCCGCGGAGTGAGCC 177  
 |||||  
 DB 181 TGGCGGTGGTGAAGAGACTCGGGAGTCTGCTCTTCCAAAGTCCCGCGCTGAGTGAGCT 240  
 |||||  
 QY 178 CTCGCCCGAGTCAGCCCAATGCTCTCTCGGCTCTCTCTGTCGACATCTGCCCTGGCC 237  
 |||||  
 DB 241 CTCACCCCGAGTCAGCCCAATGAGCTCTTCGGCTTCTCTGTCGACATCTGCCCTGGCC 300  
 |||||  
 QY 238 GGCCAAAGAACGGGAGCTCGGCTGAGTCCAACTGAGCAGCAGAGTTGAGCTCTCCAGC 297  
 |||||  
 DB 301 GGCCAGAGACAGGGAGCTCAGCGGAATCCAACTGAGTAGTAAATTCAGATTTTCCAGC 360  
 |||||  
 QY 298 GACAGGAAACAGAAACGAGTGCAGATCCCGGCTGAGAGAGTTTCTCACTATCTGTT 357  
 |||||  
 DB 361 AACAAGGAAACAGAAACGAGTGCAGATCTCTGAGTGCAGAGATTTATTTACTGTCTACT 420  
 |||||  
 QY 358 AATGGAGCATCCACAGCCCGAAGTTTCTCTATACGTACCCCAAGAAATATGGTCTGGTG 417  
 |||||  
 DB 421 AATGGAAGTATTCACAGCCCAAGTTTCTCTATCTATCTATCCAGAAATACGGTCTTGTA 480  
 |||||  
 QY 418 TGGAGATTAGTTGCACTAGATGAAATGTCCGATCCAGCTCAGTGCATTTGATGAGAGATT 477  
 |||||  
 DB 481 TGGAGATTAGTAGCAGTAGAGGAAATGATGATACAACTTACGTTTGTATGAAGATT 540  
 |||||  
 QY 478 GGCTGGAAAGATCCAGAAACAGATATATGCAAGTATGATTTGTAGAAGTTAGGAGCCC 537  
 |||||  
 DB 541 GGCTTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAGTTAGGAGCCC 600  
 |||||  
 QY 538 AGTGATGGAAGTGTGTTTGGAGCTGCTGTGGTCTCTGGGACTGTCCAGGAAAGCAGACT 597  
 |||||  
 DB 601 AGTGATGGAAGTGTGTTTGGAGCTGCTGTGGTCTCTGGTACTGTACAGGAAACAGATT 660  
 |||||  
 QY 598 TCTAAAGGAAATCATATCAGGATTAAGATTTGATCTGATGAGATTTTCCATCTGAACCC 657  
 |||||  
 DB 661 TCTAAAGGAAATCAAAATTAGGATTAAGATTTGATCTGATGAATATTTTCTCTGAACCA 720  
 |||||  
 QY 658 GGATTTGTCATCCACTACAGTATTTATCAGCCCAAGTGCACAAACCCAGAGTCTTCG 717  
 |||||  
 DB 721 GGTTTCTGATCCACTACAACTTGTCTGATGCCCAATTCACAGAGCTGTGAGTCTTCA 780  
 |||||  
 QY 718 GTCTGCCCCCTTCATCTTTGTCTATTTGGACCTGCTCAAACTGCTGTGATGCTTCCAGT 777  
 |||||  
 DB 781 GTCTACCCCCCTTCAGCTTTGCCATGAGCTGCTTAAATGCTATTAATCTGCTTAACTGCTTAGT 840  
 |||||  
 QY 778 ACCTTGGAAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC 837  
 |||||  
 DB 841 ACCTTGGAAAGCTTATTCGATATCTTGAACACAGAGATGGCAGTTGGACTTAGAGAT 900  
 |||||  
 QY 838 CTCTAAGCCCAACATGGCAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAGCAAA 897  
 |||||  
 DB 901 CTATATAGGCCCACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGGAAAAATCCAGA 960  
 |||||  
 QY 898 GTGCTGAATCTGAATCTCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAAC 957  
 |||||  
 DB 961 GTGCTGAATCTGAATCTCTCTCAAGGAGAGGTAAAGTATATACAGCTGCACACCTCTGTAAC 1020  
 |||||

QY 958 TTCTCAGTCTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGT 1017  
Db 1021 TTCTCAGTCTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGT 1080  
QY 1018 CTCCTGCTCAAGCGCTGTGGAGAAATGTGCTGTGTCTCATATTAATTCGAATGAATGT 1077  
Db 1081 CTCCTGCTTAACCGCTGTGGTGGAACTGTGCCCTGTGTCTCCACAATTCGAATGAATGT 1140  
QY 1078 CAGTGTCTCCACGTAAGTACAAAAGTACATGAGTCTCTCAGTTGAGACCAAAA 1137  
Db 1141 CAATGTGTCTCCACGTAAGTACAAAAGTACATGAGTCTCTCAGTTGAGACCAAAA 1200  
QY 1138 ACTGGAGTCAAGGATTTGATAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAA 1197  
Db 1201 ACCGGTGTGAGGGATTTGACAAATCACTCACCAGGTGGCCCTGGAGCAACATGAGGAG 1260  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTAACTGCGAGCTTGTGAGACGAC 1254  
Db 1261 TGTGACTGTGTGTGAGAGGAGGACAGAGGAGTAGCGGCATCACACGAGCAGCTC 1317

RESULT 12  
ID ABS57294  
XX ABS57294 standard; DNA; 2825 BP.  
AC ABS57294;  
XX  
DT 31-JAN-2003 (first entry)  
XX  
DE DNA encoding human vascular endothelial cell growth factor-E (VEGF-E).  
XX Human; vascular endothelial cell growth factor-E; VEGF-E; PRO:200;  
KW VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration;  
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;  
KW cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis;  
KW cardiant; cytostatic; antidiabetic; antiarteriosclerotic;  
KW gene therapy; gene; ds.  
XX  
XX Homo sapiens.  
XX

Key Location/Qualifiers  
FT 259..1296  
CDS /\*tag= a  
FT /\*product= "VEGF-E"  
XX  
PN US6455283-B1.  
XX  
PD 24-SEP-2002.  
XX  
PF 10-MAR-1999; 99US-0265686.  
XX  
PR 17-MAR-1998; 98US-0040220.  
PR 02-NOV-1998; 98US-0184216.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ferrara N, Kuo SS;  
XX  
XX WPI; 2003-066231/06.  
DR P-PSDB; ABG72132.  
XX  
XX New nucleic acid encoding endothelial cell growth factor-E polypeptide,  
PT useful for diagnosing or treating a cardiovascular, endothelial or  
PT angiogenic disorder such as cancer, diabetes mellitus or  
PT atherosclerosis -  
XX  
XX Claim 2; Fig 1; 46pp; English.  
XX  
XX The present invention relates to the isolation of human vascular  
CC endothelial cell growth factor-E (VEGF-E, also referred to as  
CC PRO:200), and the polynucleotide sequence encoding it. VEGF-E is  
CC related to VEGF and bone morphogenetic protein 1. VEGF-E is useful

CC in wound repair, as well as in the generation and regeneration of  
CC tissue. The sequences of the invention are useful for diagnosing or  
CC treating cardiovascular, endothelial or angiogenic disorders such as  
CC cancer, diabetes mellitus, cardiac hypertrophy and atherosclerosis.  
CC The polynucleotide encoding VEGF-E is useful in the gene therapy of  
CC such disorders. The present sequence encodes human VEGF-E.  
XX  
XX Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;  
Query Match 62.0%; Score 914.2; DB 25; Length 2825;  
Best Local Similarity 83.5%; Pred. No. 1.7e-267;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGAGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAACATA 61  
Db 61 AACTGAGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAACATA 120  
QY 62 CCTCGGATTTCTGCTGCCAGAGCGCGCCAGCGGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 121 CCTCGGATTTCTGCTGCCAGAGCGGGCTCGCGCTTCCACCCAGTGGAGCTTTCCC 180  
QY 122 CGG- ---GCTGGGCTGAGCCTTCGAGTGTGCTTCCCGAGTCCCGCCGAGTGAAGCC 177  
Db 181 TGGCGGTGTGAAAGAGACTCGGGAGTGTGCTTCCAAAGTGCCTCCCGCTGAGTGAAGCT 240  
QY 178 CTCGCCCCAGTCAAGCCAAATGCTCTCTCGGCTCTCTCTGTGCAATGTGCCCTGGCC 237  
Db 241 CTCACCCCGAGTCAAGCCAAATGAGCTCTCTCGGCTCTCTCTGTGCAATGTGCCCTGGCC 300  
QY 238 GGCCTAAGAACGGGAGTCTGGGCTGAGTCCAACTGAGCAGCAAGTTCGAGCTTCACGC 297  
Db 301 GGCCTAAGAACGGGAGTCTGAGGGGAAATCCAACTGAGTAAATTTCCAGTTTTCAGC 360  
QY 298 GACAAAGAACAGAGCGAGTGCAGATCCCGGATCAGAGAGTGTGCTATATCTCGGT 357  
Db 361 AACAAAGAACAGAGCGAGTGCAGATCCCGGATCAGAGAGTGTGCTATATCTCGTCTACT 420  
QY 358 AATGGGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAGAAATATGCTGCTGGTG 417  
Db 421 AATGGAGTATTACAGCCCAAGGTTTCTCTCATACTTATCCAGAAATACGGTCTTGTA 480  
QY 418 TGGAGATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATT 477  
Db 481 TGGAGATTAGTTCAGTAGAGGAAATGTATGGATACAACCTTACCTTTGATGAAAGATT 540  
QY 478 GGCCTGGAAGATCCAGAGAGCATATATGCAAGTATGATTTTGTAGAGTTGAGAGGCC 537  
Db 541 GGCCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGAGGCC 600  
QY 538 AGTGATGGAAGTGTTTTGGAGCGCTGTGTGTTCTGGGACTGTGCCAGGAAAGCAGACT 597  
Db 601 AGTGATGGAACATATATTAGGGCGCTGTGTGTTCTGGTACTGTACCAGGAAACAGATT 660  
QY 598 TCTAAGGAAATCATATCAGATAGAGTATGTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 661 TCTAAGGAAATCAATTAGGATAAGATTTGTATCTGATGAATATTTTCTCTTGAACCA 720  
QY 658 GGATTCGCAATCCACTACAGTATTATCATGCAAGTTCACAGAAACACAGAGTCTTCG 717  
Db 721 GGGTTCTGCATCCACTACAAATGTATGCCAATTCACAGAGCTGTGAGTCTTCA 780  
QY 718 GTGTTCGCCCTTCATCTTTGTATGAGCCTGTCAACATGTGTGACTGCTTCAGT 777  
Db 781 GTGTCTACCCCTTCAGCTTTGCCACTGACTGCTTAATATGCTATAAATGCTCTTGTAGT 840  
QY 778 ACCTTGAAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGGTGGACTTGGACAGC 837  
Db 841 ACCTTGAAGAGCTTATTTCGATATCTTGAACACAGAGATGGCAGTTGGAGATTGAAGAT 900  
QY 838 CTCTACAGCAACATGCGAGCTTTTGGCAAGGCTTTTCTGTATGGGAAAAAGCAAA 897  
Db 901 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAATTCAGA 960

QY 898 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAAC 957  
Db 961 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1020  
QY 958 TTCTCAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT 1017  
Db 1021 TTCTCAGTGTCCATACCGGAAGAGCTAAAGAGGACCGATACCATATTCTGGCCAGGTTGT 1080  
QY 1018 CTCTGCTCAAGCGCTGTGGAGGAAATTTGCTGTTGTTCTCTCCATATTGCAATGAATGT 1077  
Db 1081 CTCTGTTTAAACGCTGTGGGAACTGTGCTGTTGTTCTCTCCATATTGCAATGAATGT 1140  
QY 1078 CAGTGTGTCCACGATTAAGTTTACAAAAGATGACATGAGGTCTCTCAGTTGAGACCAAAA 1137  
Db 1141 CAATGTGTCCACGATTAAGTTTACAAAAGATGACATGAGGTCTCTCAGTTGAGACCAAAA 1200  
QY 1138 ACTGGAGTCAAGGATTCATTAAGTCACTCACTGATGTTGCTCTGGACACACGAGAA 1197  
Db 1201 ACCGTGTGTCAGGATTCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAG 1260  
QY 1198 TGTGACTGTGTGTAGAGGAAACGACGAGGAGTAACTGACAGCTTCTGTAGCAGCAC 1254  
Db 1261 TGTGACTGTGTGTAGAGGAGGACACGAGGATAGCCGATCACCACGAGCTC 1317

RESULT 13  
AAD06812  
ID AAD06812 standard; DNA; 2827 BP.  
XX AC AAD06812;  
XX DT 10-AUG-2001 (first entry)  
XX DE Human LP8, a PDGF-related protein encoding DNA.  
XX KW Human; LP8; platelet-derived growth factor-related protein; PDGF  
KW cytosolic; vulnery; bone growth; therapy; bone fracture;  
KW prophyaxis; osteoblast proliferation; osteoporosis; muscle loss;  
KW bone loss; endocrine disorder; arthritis; sarcopenia;  
KW periodontal disease; cartilage differentiation; wound healing; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 276..1313  
XX FT /\*tag= a  
XX FT /product= "Human LP8, a PDGF-related protein"  
XX PN WO200132197-A2.  
XX PD 10-MAY-2001.  
XX PE 24-OCT-2000; 2000WO-US26272.  
XX PR 02-NOV-1999; 99US-0163056.  
XX PR 02-NOV-1999; 99US-0163203.  
XX PR 02-NOV-1999; 99US-0163204.  
XX PA (ELIL ) LILLY & CO ELI.  
XX PI Hock JM, Na S, Hammond LJ, Kharitonov A, Krishnan V, Becker GW;  
XX WPI; 2001-316384/33.  
XX DR P-PSDB; AAE02649.  
XX DR  
XX PT New LP8 protein or its fragment for promoting bone growth, treating  
PT bone fractures, increasing or maintaining bone density, and treating  
PT osteoporosis, arthritis, sarcopenia and periodontal disease -  
XX PS Example 1; Page 57-59; 61pp; English.  
XX PS  
XX CC The present sequence is a DNA encoding human LP8, platelet-derived  
CC growth factor (PDGF)-related protein or its fragment. LP8 or its

CC fragment is useful for promoting bone growth, treating bone fractures,  
CC prophylactically increasing or maintaining bone density in a subject  
CC having a substantially normal bone density, so as to stimulate  
CC osteoblast proliferation, treating osteoporosis, muscle or bone loss  
CC due to malignancy, endocrine disorder, arthritis, sarcopenia and  
CC periodontal disease, preventing cartilage differentiation, and  
CC wound healing.  
XX

SQ Sequence 2827 BP; 864 A; 522 C; 589 G; 852 T; 0 other;

Query Match 62.0%; Score 914.2; DB 22; Length 2827;  
Best Local Similarity 83.5%; Pred. No. 1.7e-267;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGGAAACTA 61  
Db 78 AACTGGATACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGGAAACTA 137  
QY 62 CCCTGCGATTCTCTGCTGCCAGAGCCGCGGCTTCCACCGCAGCGAGCTTTCC 121  
Db 138 CCCTGCGATTCTCTGCTGCCAGAGAGGCTCGGGCTTCCACCGCAGCGCTTTCC 197  
QY 122 CGG---GCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCC 177  
Db 198 TGGCGTGTGAAGAGACTCGGGAGTCTGCTTCCAAAGTCCCGCGCTGAGTGAGCT 257  
QY 178 CTGCCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCC 237  
Db 258 CTCACCCAGTCAGCCAAATGAGCTCTTCCGGCTCTCTCTGCTGACATCTGCCCTGGCC 317  
QY 238 GGCCTGAGGAGCTCGGCTGAGTCCACCTGAGCAGCAGTTCGAGCTCTCCAGC 297  
Db 318 GGCCTGAGGAGCTCGGCTGAGTCCACCTGAGTGAATTCAGTTTCCAGC 377  
QY 298 GACAGGAAACAGACGAGTGCAGATCCCGGCTAGAGAGTGTCTCATATCTGT 357  
Db 378 AACAGGAAACAGACGAGTGCAGATCCAGATCTGAGAGATTTATTCTGTCTACT 437  
QY 358 AATGGAGATCCACAGCCCGAGTTCTCTATGTTACCCAGAAATATGTTGCTGTG 417  
Db 438 AATGGAAGTATTCACAGCCCGAGTTCTCTATCTTATCCAGAAATACGGTCTTGGTA 497  
QY 418 TGGAGATTAGTTCAGTATGAAATGTGCGGATCCAGCTGACATTTGATCAGAGATT 477  
Db 498 TGGAGATTAGTTCAGTATGAAATGTGCGGATCCAGCTGACATTTGATCAGAGATT 557  
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 XX  
 AC AAA47452;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE Human TANGO 128 coding sequence.  
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 KW TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;  
 KW graft versus-host diseases; rheumatoid arthritis; psoriasis;  
 KW inflammatory bowel disease; septic shock; ulcerative colitis;  
 KW Crohn's disease; chronic myelogenous leukemia; cancer; liver  
 KW disease; Hodgkin's disease; osteoarthritis; Lyme's disease;  
 KW cachexia; autoimmune disease; myasthenia gravis; autoimmune diabetes;  
 KW systemic lupus erythematosus; transgenic animal; diagnosis;  
 KW prognosis; prophylactic; therapeutic; human; ds.  
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 OS Homo sapiens.  
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 FT CDS 288..1325  
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 XX  
 PN WO200039284-A1.  
 XX  
 PD 06-JUL-2000.  
 XX  
 PF 23-DEC-1999; 99WO-US31025.  
 XX  
 PR 30-DEC-1998; 98US-0223546.  
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 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Holtzman DA;  
 PI  
 XX WPI; 2000-465743/40.  
 DR P-PSDB; AAB01419.  
 DR  
 XX Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,  
 PT 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid  
 PT arthritis, psoriasis and autoimmune diseases  
 XX  
 XX Claim 1; Fig 1; 209pp; English.  
 PS  
 XX

CC Nucleic acids encoding TANGO polypeptides are useful as modulating  
 CC agents for regulating cellular processes like asthma, graft  
 CC versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory  
 CC bowel disease, septic shock, ulcerative colitis, Crohn's disease,  
 CC chronic myelogenous leukemia, cancer, liver disease, Hodgkin's  
 CC disease, osteoarthritis, Lyme's disease, cachexia and autoimmune  
 CC diseases e.g. myasthenia gravis, autoimmune diabetes and systemic  
 CC lupus erythematosus. The nucleic acids are also useful for producing  
 CC transgenic animals and the TANGO polypeptides themselves. Partial  
 CC TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in  
 CC forensic biology, for diagnostic assays, prognostic assays,  
 CC pharmacogenomics and for monitoring clinical trials. TANGO  
 CC polypeptides are suitable for both prophylactic and therapeutic  
 CC methods for treating a subject at risk of a disorder or having a  
 CC disorder associated with aberrant TANGO expression. A wide range  
 CC of cellular disorders can be treated.  
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 SQ Sequence 2839 BP; 858 A; 532 C; 600 G; 849 T; 0 other;  
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QY      838 CTCTAAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAA 897
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QY      1018 CTCCTGGTCAAGCGCTGTGGAGGAAATTTGCTGCTGTGTCTCCATATTTGCAATGAATGT 1077
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AC      AAZ34296;
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DT      07-DEC-1999 (first entry)
DE      Human PRO200 nucleotide sequence.
KW      Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW      probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW      secreted protein; transmembrane protein; ss.
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PN      WO9946281-A2.
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XX	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	Db	747	GGTTTCTGCATCCACTACAACTTGTCTGTCACCAATTCACAGAGCTGTGAGTCTCTTCA	806
DR	WPI; 1999-551358/46.	QY	718	GTGTTGCCCTTTCATCTTTTGTTCATTTGGACCTGCTCAACAACTGCTGTGATGCTTTCAGT	777
XX	P-PSDB; AAY41766.	Db	807	GTGCTACCCCTTTCAGCTTTTGGCAGTGGACCTGCTTAATAATGCTATACTGCTTTCAGT	866
PT	New secreted and transmembrane polypeptides and their polynucleotides,	QY	778	ACCTTGGAAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTTGGACAGC	837
PT	useful for treating blood coagulation disorders, cancers and cellular	Db	867	ACCTTGGAAAGAGCTTATTCGATCTTGAACAGAGAGATGGCAGTTGGACTTAGAAGAT	926
PT	adhesion disorders -	QY	838	CTCTACAAGCCCAACATGGCAGCTTTTGGCAAGCTTTCTCTGATGGGAAAAAAGCAAA	897
XX	Claim 2; Fig 206; 530pp; English.	Db	927	CTATATAGGCCAACTTTGGCAACTTCTTGGCAAGCTTTTCTTTTGGAAAGAAAATCCAGA	986
XX	The present invention describes secreted and transmembrane polypeptides	QY	898	GTGCTGAATCTGAATCTCTCTCAAGGAGAGGTTAAACTCTACAGCTGCACACCCCGAAC	957
CC	and their polynucleotides. The nucleotide sequences are useful as	Db	987	GTGCTGGATCTGAACCTTCTTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAAC	1046
CC	sources of probes, primers, for chromosome mapping, and for generation	QY	958	TTCTCAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGT	1017
CC	of antisense sequences. They can also be used to create transgenic	Db	1047	TTCTCAGTGTCCATAGGAGGAGAACTTAAGAGAACCGATACCAATTTCTGGCCAGGTTGT	1106
CC	animals. The proteins can be used to treat a variety of diseases and	QY	1018	CTCTCTGTCGAAGCGCTGTGGAGGAAATTTGTGCTGTGTCTCCATATTTGCAATGAATGT	1077
CC	disorders, depending on their function. Diseases that may be treated	Db	1107	CTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCACAAATTCGAATGAATGT	1166
CC	include blood coagulation disorders, cancers and cellular adhesion	QY	1078	CAGTGTGTCCACGTTAAAGTTACAAAAGTACATGAGGTCTCTCAGTTGAGACCAAAA	1137
CC	disorders. They may also be used to raise antibodies. AAZ33891 to	Db	1167	CAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAAGGTCTCTCAGTTGAGACCAAAAG	1226
CC	AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and	QY	1138	ACTGGAGTCAAGGGATTTCATTAAGTCACTCACTGATGTGCTCTGGAACACCAACGAGAA	1197
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XX	invention.	QY	1198	TGTGACTGTGTGTAGAGGAAACGACAGGAGGGTAACTGCAGGCTTCTGTAGCAGCAC	1254
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Job time : 276.163 secs

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Db	447	AATGGAAGTATTCACAGCCCAAGTTTCTCTATATTCAGAAATATACGGTCTTGSTA	506				
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Db	567	GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGAACCC	626				
QY	538	AGTGATGAAGTGTGTTAGACGCTGTGTGTTTCTGGGCTGTGCGGAGCAAGCACT	597				
Db	627	AGTGATGAAGTGTGTTAGACGCTGTGTGTTTCTGGGCTGTGCGGAGCAAGCACT	686				
QY	598	TCATAAGGAATCATATCAGATGAATTTGTATCTGATGATATTTTCCATCTGACCC	657				



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 569978 seqs, 220691566 residues

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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6	878.8	59.6	1760	4	US-09-564-595D-32
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8	878.8	59.6	1764	4	US-09-457-066-1
9	745.8	50.6	1095	4	US-09-457-066-50
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13	137.2	9.3	1110	4	US-09-564-595D-6
14	137.2	9.3	1472	4	US-09-540-224-3
15	137.2	9.3	1472	4	US-09-564-595D-52
16	125.6	8.5	1910	4	US-09-457-066-36
17	123.2	8.4	1882	4	US-09-540-224-1
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23	36.2	2.5	1806	4	US-09-351-229-3
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c	31	34.4	2.3	1560	4	US-09-252-991A-166	Sequence 166, App
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c	33	34.4	2.3	1803	4	US-09-252-991A-170	Sequence 170, App
c	34	34.4	2.3	2610	4	US-09-252-991A-175	Sequence 175, App
c	35	34.2	2.3	77536	4	US-09-410-551B-1	Sequence 1, Appli
c	36	34	2.3	501	4	US-09-252-991A-1347	Sequence 1347, Ap
c	37	34	2.3	582	4	US-09-252-991A-1257	Sequence 1257, Ap
c	38	34	2.3	1370	3	US-09-111-470-9	Sequence 9, Appli
c	39	34	2.3	1458	3	US-09-040-220D-4	Sequence 3, Appli
c	40	33.6	2.3	40	4	US-09-265-686-4	Sequence 4, Appli
c	41	33.6	2.3	40	4	US-09-704-139-3	Sequence 3, Appli
c	42	33.6	2.3	531	4	US-09-704-139-3	Sequence 3, Appli
c	43	33.6	2.3	1390	4	US-09-704-139-1	Sequence 1, Appli
c	44	33.6	2.3	1424	1	US-08-403-634-3	Sequence 3, Appli
c	45	33.6	2.3	1424	3	US-08-913-441B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-564-595D-34  
; Sequence 34, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-564-595D-34

Query Match	98.0%;	Score 1444.8;	DB 4;	Length 3571;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 1460;	Conservative 0;	Mismatches 8;	Indels 1;	Gaps 1;
Qy	2	ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGGAACTA	61	
Db	856	AACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGGAACTA	915	
Qy	62	CCCTGCGATTCTTGTGTCAGAGCCGGCCAGGCGCTTCCACCGAGCGAGCCCTTCCC	121	
Db	916	CCCTGCGATTCTTGTGTCAGAGCCGGCCAGGCGCTTCCACCGAGCGAGCCCTTCCC	975	
Qy	122	CGGGCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	181	
Db	976	C-GGCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	1034	
Qy	182	CCCAGTTCAGCAAAATGCTCTCTCCGCGCTCTCTCTGTCACATCTGCGCCGCGCC	241	
Db	1035	CCCAGTTCAGCAAAATGCTCTCTCCGCGCTCTCTCTGTCACATCTGCGCCGCGCC	1094	
Qy	242	AAAGACGGGAGTTCGGGCTGAGTCCAACTGAGCAGAGTTCAGCTCTCCAGCGACA	301	

Db 1095 AAAGACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACGGAGTCAAGATCCCGGCATGAGAGAGTGTCACTATATCTGTTAATG 361  
Db 1155 AGGAACAGAACGGAGTCAAGATCCCGGCATGAGAGAGTGTCACTATATCTGTTAATG 1214  
Qy 362 GGAGCATCCACAGCCGGAAGTTCTCATACGTACCCAAAGAAATATGTTGCTGTTGGA 421  
Db 1215 GGAGCATCCACAGCCGGAAGTTCTCATACATACCCAAAGAAATATGTTGCTGTTGGA 1274  
Qy 422 GATTAGTTGAGTATGATAAATGTCGGATCCGATCCAGCTGACATTTGATGAGAGATTGGGC 481  
Db 1275 GATTAGTTGAGTATGATAAATGTCGGATCCGATCCAGCTGACATTTGATGAGAGATTGGGC 1334  
Qy 482 TGGAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCAGTG 541  
Db 1335 TGGAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCAGTG 1394  
Qy 542 ATGAAAGTGTATAGACGCTGGTGTGTTCTGGACCTGTCGCCAGGAAAGCAGACTTCTA 601  
Db 1395 ATGAAAGTGTATAGACGCTGGTGTGTTCTGGACCTGTCGCCAGGAAAGCAGACTTCTA 1454  
Qy 602 AAGGAATCATATCAGATATGATTTGATCTGATGATATTTTCCATCTGAACCCGAT 661  
Db 1455 AAGGAATCATATCAGATATGATTTGATCTGATGATATTTTCCATCTGAACCCGAT 1514  
Qy 662 TCTGCATCCACTACAGTATATATGTCACCAAGTCACAGAAACACAGAGTCTTCGSGTG 721  
Db 1515 TCTGCATCCACTACAGTATATATGTCACCAAGTCACAGAAACACAGAGTCTTCGSGTG 1574  
Qy 722 TGCCCCCTTCATCTTGTGATGACCTGCTCAACATGCTGTGATGCTTCAGTACCT 781  
Db 1575 TGCCCCCTTCATCTTGTGATGACCTGCTCAACATGCTGTGATGCTTCAGTACCT 1634  
Qy 782 TGGAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGTGGACTTGGACAGCTCT 841  
Db 1635 TGGAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGTGGACTTGGACAGCTCT 1694  
Qy 842 ACAAGCCAACTGACGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAACTGACGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1754  
Qy 902 TGATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGGAACTTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGGAACTTCT 1814  
Qy 962 CAGTGTCCATACGGGAAGAGCTAAAGAGCAGATACCATATCTGGCCAGTTGTCTCC 1021  
Db 1815 CAGTGTCCATACGGGAAGAGCTAAAGAGCAGATACCATATCTGGCCAGTTGTCTCC 1874  
Qy 1022 TGGTCAAGCGCTGGAGGAAATTTGTCCTGTTCTCCATAATGCAATGAATGTCAGT 1081  
Db 1875 TGGTCAAGCGCTGGAGGAAATTTGTCCTGTTCTCCATAATGCAATGAATGTCAGT 1934  
Qy 1082 GTGTCCACGCTAAAGTTACAAAAGTACCATGAGTCCCTCAGTTGAGACCAAAACTG 1141  
Db 1935 GTGTCCACGCTAAAGTTACAAAAGTACCATGAGTCCCTCAGTTGAGACCAAAACTG 1994  
Qy 1142 GAGTCAAGGATTCATAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 1201  
Db 1995 GAGTCAAGGATTCATAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 2054  
Qy 1202 ACTGTGTGTAGAGGAAACGACAGAGGTAATCTGACGCTTCGTAGCAGCACAGTGAG 1261  
Db 2055 ACTGTGTGTAGAGGAAACGACAGAGGTAATCTGACGCTTCGTAGCAGCACAGTGAG 2114  
Qy 1262 CACTGGCATCTGTGATCCCCCAACAGCACTTCATCCCCACAGGTTGGCCGAGGG 1321  
Db 2115 CACTGGCATCTGTGATCCCCCAACAGCACTTCATCCCCACAGGTTGGCCGAGGG 2174  
Qy 1322 CTCTCAGCTGTGATGCTGGCTATGGTAAAGATCTTACTGTCTCCAAACCAAAATTTCTCAG 1381

Db 2175 CTCTCAGCTGTGATGCTGGCTATGGTAAAGATCTTACTCTCTCCAAACCAAAATTTCTCAG 2234  
Qy 1382 TTGTTTGTCTCAATAGCTTCCCTCTCAGGACTTCAAGTGTCTTCTTAAAGACCCAGAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCTTCCCTCTCAGGACTTCAAGTGTCTTCTTAAAGACCCAGAGGC 2294  
Qy 1442 ACCAANAGGAGTCAATCACAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCACAAGCACTGC 2323  
RESULT 2  
US-09-706-968-42  
; Sequence 42, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049) ... (2086)  
US-09-706-968-42  
Query Match 98.0%; Score 1444.8; DB 4; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
Qy 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 856 AACTGGAGACACAGAGAGGCTCTAGGAAAAAATTTTGGATGGGATTTATGTGAAACTA 915  
Qy 62 CCCTGCCATTTCTGTCTGCCAGAGCCCGGCGGCTTCCACCGCAGCGAGCCTTTCCC 121  
Db 916 CCCTGCCATTTCTGTCTGCCAGAGCCCGGCGGCTTCCACCGCAGCGAGCCTTTCCC 975  
Qy 122 CGGCTGGGCTGAGCCTTGGAGTGGTCTTCCAGTGGCCGCGGAGTGGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCTTGGAGTGGTCTTCCAGTGGCCGCGGAGTGGAGCCCTCG 1034  
Qy 182 CCCAGTCAAGCAAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCCCCGCGGCC 241  
Db 1035 CCCAGTCAAGCAAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCCCCGCGGCC 1094  
Qy 242 AAGAACCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 301  
Db 1095 AAGAACCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACGGAGTCAAGATCCCGGCATGAGAGAGTGTCACTATATCTGTTAATG 361  
Db 1155 AGGAACAGAACGGAGTCAAGATCCCGGCATGAGAGAGTGTCACTATATCTGTTAATG 1214  
Qy 362 GGAGCATCCACAGCCGGAAGTTCTCATACGTACCCAAAGAAATATGTTGCTGTTGGA 421  
Db 1215 GGAGCATCCACAGCCGGAAGTTCTCATACATACCCAAAGAAATATGTTGCTGTTGGA 1274  
Qy 422 GATTAGTTGAGTATGATAAATGTCGGATCCAGCTGACATTTGATGAGAGATTGGGC 481

1275	Db	GA	TTAGTTG	CAGTAGATG	AAATTTG	CCGATCCAG	CTGACATTTG	ATGAGATTTGGG	C	1334
482	Qy	TGG	AAGATCC	AGACGATATATG	CAAGTATGATTTT	GTAGAAGTTG	AGAGCCAGTG	G	541	
1335	Db	TGG	AAGATCC	AGACGATATATG	CAAGTATGATTTT	GTAGAAGTTG	AGAGCCAGTG	C	1394	
542	Qy	ATG	AAAGTGT	TTTAGG	ACGTGTGTGG	ATCTGGGATGTG	CCAGAAAGCAGACTTCTA	G	601	
1395	Db	ATG	AAAGTGT	TTTAGG	ACGTGTGTGG	ATCTGGGATGTG	CCAGAAAGCAGACTTCTA	C	1454	
602	Qy	AAG	AAATCATATC	AGATTAAGATTTT	GTATCTGATGAGTATTTT	CCATCTG	AAACCCGAT	G	661	
1455	Db	AAG	AAATCATATC	AGATTAAGATTTT	GTATCTGATGAGTATTTT	CCATCTG	AAACCCGAT	C	1514	
662	Qy	TCTG	ATCCACTAC	AGTATTATCATG	CCACAAAGTCA	CAGAAAC	CCAGGTCCTTCGGTGT	G	721	
1515	Db	TCTG	ATCCACTAC	AGTATTATCATG	CCACAAAGTCA	CAGAAAC	CCAGGTCCTTCGGTGT	C	1574	
722	Qy	TG	CCCCCTTCA	TCTTTGTCA	TGTGA	CCCTGCTCA	CAATGCTGTGA	CTG	781	
1575	Db	TG	CCCCCTTCA	TCTTTGTCA	TGTGA	CCCTGCTCA	CAATGCTGTGA	C	1634	
782	Qy	TGG	AAGACTG	ATTTCCG	TACTAGAC	CCAGATCGATG	GCAGGTGGA	CTT	841	
1635	Db	TGG	AAGACTG	ATTTCCG	TACTAGAC	CCAGATCGATG	GCAGGTGGA	C	1694	
842	Qy	ACA	AGCCAACTG	GCAGCTTTT	TGGC	CAAGGCTTTT	CCTGTATG	G	901	
1695	Db	ACA	AGCCAACTG	GCAGCTTTT	TGGC	CAAGGCTTTT	CCTGTATG	C	1754	
902	Qy	TGA	ATCTGA	ATCTCTCA	AGGAAGGTAA	AACCTC	TACAGCTG	CA	961	
1755	Db	TGA	ATCTGA	ATCTCTCA	AGGAAGGTAA	AACCTC	TACAGCTG	C	1814	
962	Qy	CAG	TGTCATAC	GGGAAGAGCT	TAAAGAGCAGAT	TACCATATCT	GTG	CC	1021	
1815	Db	CAG	TGTCATAC	GGGAAGAGCT	TAAAGAGCAGAT	TACCATATCT	GTG	C	1874	
1022	Qy	TGG	TCAAGCGCT	TGTGG	AGAAATGTG	CGCTTGTCT	CCATAATG	CA	1081	
1875	Db	TGG	TCAAGCGCT	TGTGG	AGAAATGTG	CGCTTGTCT	CCATAATG	C	1934	
1082	Qy	GTG	TCCCAGTAA	AGTTACAA	AAAGTAC	ATAGAGTCTT	CAGTTG	AG	1141	
1935	Db	GTG	TCCCAGTAA	AGTTACAA	AAAGTAC	ATAGAGTCTT	CAGTTG	C	1994	
1142	Qy	GAG	TCAAGGAT	TGCAT	TAAGTCACT	GTATGTGG	CTCTG	GA	1201	
1995	Db	GAG	TCAAGGAT	TGCAT	TAAGTCACT	GTATGTGG	CTCTG	C	2054	
1202	Qy	ACT	GTGTGTG	TAGAGG	AAACG	CAGAGG	GTAACTG	AC	1261	
2055	Db	ACT	GTGTGTG	TAGAGG	AAACG	CAGAGG	GTAACTG	C	2114	
1262	Qy	CAC	TGGCATCT	GTGTAC	CCCCAC	AGCAAC	CTTCC	CA	1321	
2115	Db	CAC	TGGCATCT	GTGTAC	CCCCAC	AGCAAC	CTTCC	C	2174	
1322	Qy	CTC	TACGCTG	ATGCTGG	CTATG	GTAAAGATCTT	ACTG	CT	1381	
2175	Db	CTC	TACGCTG	ATGCTGG	CTATG	GTAAAGATCTT	ACTG	C	2234	
1382	Qy	TTG	TTTGTCTT	CAATAG	CCCTTCC	CCGAGG	ACTTCA	AG	1441	
2235	Db	TTG	TTTGTCTT	CAATAG	CCCTTCC	CCGAGG	ACTTCA	C	2294	
1442	Qy	ACC	AAAGAGTCA	TCAATCA	AAAGCA	CTGC			1470	
2295	Db	ACC	AAAGAGTCA	TCAATCA	AAAGCA	CTGC			2323	

### RESULT 3

```

US-09-457-066-42
; Sequence 42, Application US/09457066
; Patent NO. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: fastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049) ... (2086)
US-09-457-066-42

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Query Match	97.2%;	Score 1432.8;	DB 4;	Length 3573;
Best Local Similarity	99.3%;	Pred. No. 0;	8;	Indels 3; Gaps 2;
Matches 1460;	Conservative 0;	Mismatches		
QY	2	ACCTGGAGACACAGAGGGCTCTAGCAAAAATTTTGGATGGGATATATGTGGAAACTA	61	
DB	856	AAC TGGAGACACAGAGGGCTCTAGCAAAAATTTTGGATGGATATATGTGGAAACTA	915	
QY	62	CCCTGGGATTCCTGTGTCAGAGCCGGGCGAGGCGCTTCCACCCGACGGCAGCCTTTCCC	121	
DB	916	CCCTGCGATTCCTGTGTCAGAGCCGGGCGAGGCGCTTCCACCCGACGGCAGCCTTTCCC	975	
QY	122	CGGGCTGGGCTGAGCCTTTGGAGTGGTGGCTTCCCAGTGGCCGGCGGAGTAGAGCCCTCG	181	
DB	976	C-GGCTGGGCTGAGCCTTTGGAGTGGTGGCTTCCCAGTGGCCGGCGGAGTAGAGCCCTCG	1034	
QY	182	CCCCAGTCAGCAAAATGCTCTCTCCCTGGGCTCTCTCTGTGACATCTGCCCTGGCGCGCC	241	
DB	1035	CCCCAGTCAGCAAAATGCTCTCTCCCTGGGCTCTCTCTGTGACATCTGCCCTGGCGCGCC	1094	
QY	242	AAAGAACCGGGACCTCGGCTCAGTCCCAACCTGACGACGACAGTTCGAGCTCTCCAGCGACA	301	
DB	1095	AAAGAACCGGGACCTCGGCTCAGTCCCAACCTGACGACGACAGTTCGAGCTCTCCAGCGACA	1154	
QY	302	AGGAACAGAACGGAGTCAAGATCCC CGGACATGAGAGAGTTGTCACTATATCTCGTAAATG	361	
DB	1155	AGGAACAGAACGGAGTCAAGATCCC CGGACATGAGAGAGTTGTCACTATATCTCGTAAATG	1214	
QY	362	GGAGCATCCACAGCCCGAGTTTCTCTCATAGTACCCCAAGAAAATATGCTGCTGTGCGGA	421	
DB	1215	GGAGCATCCACAGCCCGAGTTTCTCTCATAGTACCCCAAGAAAATATGCTGCTGTGCGGA	1274	
QY	422	GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGCACATTTGATGAGAGATTTGGGC	481	
DB	1275	GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGCACATTTGATGAGAGATTTGGGC	1334	
QY	482	TGGAAGATCCAGAACGATATATGCAAGATATGATTTGTAGAAAGTTGAGGAGCCGATG	541	
DB	1335	TGGAAGATCCAGAACGATATATGCAAGATATGATTTGTAGAAAGTTGAGGAGCCGATG	1394	
QY	542	ATGGAAGTGTGTTTTAGGACGCTGCTGGTTCCTGGGACCTGTGCCAGGAAAGCAGACTTCTA	601	
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QY	602	AAGGAAATCATATCAGGATAAGANTTGTATCTGATGAGTATTTTCCATCTGAAACCCGAT	661	
DB	1455	AAGGAAATCATATCAGGATAAGANTTGTATCTGATGAGTATTTTCCATCTGAAACCCGAT	1514	

662 TCTGATCCACTACAGTATTATCATGCCACAAGTACAGAAACACAGAGTCCTTCGGTGT 721  
Db TCTGATCCACTACAGTATTATCATGCCACAAGTACAGAAACACAGAGTCCTTCGGTGT 1574  
722 TGCCCCCTTCATCTTTGTTCATTTGACCTGCTCAACAAATGCTGTGACTGCTTCAGTACCT 781  
Db TGCCCCCTTCATCTTTGTTCATTTGACCTGCTCAACAAATGCTGTGACTGCTTCAGTACCT 1634  
782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGTGGACTTGGACAGCTCT 841  
Db TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGTGGACTTGGACAGCTCT 1694  
842 ACAAGCCAACTGCGAGCTTTGGCAAGCTTTCTGTATGGGAAAAAACAAGTGG 901  
Db ACAAGCCAACTGCGAGCTTTGGCAAGCTTTCTGTATGGGAAAAAACAAGTGG 1754  
902 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAACTCT 961  
Db TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAACTCT 1814  
962 CAGTGTCCATAGGGAAGCTTAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021  
Db CAGTGTCCATAGGGAAGCTTAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1874  
1022 TGGTCAAGCGCTGTGGAGGAATTTGTCCTGTTCTCCATAATTTGCAATGAATGTCACT 1081  
Db TGGTCAAGCGCTGTGGAGGAATTTGTCCTGTTCTCCATAATTTGCAATGAATGTCACT 1934  
1082 GTGTCCACGCTAAAGTTACAAAAAGTACCATGAGTCTCTTCACTTTGAGACCAAAAATG 1141  
Db GTGTCCACGCTAAAGTTACAAAAAGTACCATGAGTCTCTTCACTTTGAGACCAAAAATG 1994  
1142 GAGTCAAGGATGCTAAGTCACTCACTGATGTGCTCTGAAACACCAAGGAAATG 1201  
Db GAGTCAAGGATGCTAAGTCACTCACTGATGTGCTCTGAAACACCAAGGAAATG 2054  
1202 ACTGTGTGTAGAGAAACGAGGAGGTAACTGAGCTCTCGTAGCAGCACACCTGAG 1261  
Db ACTGTGTGTAGAGAAACGAGGAGGTAACTGAGCTCTCGTAGCAGCACACCTGAG 2114  
1262 CACTGCTATCTGTGTACCCCC--ACAAGAACCTTCATCCCCACAGCGTTGGCCGAG 1319  
Db CACTGCTATCTGTGTACCCCCCLYACAAGAACCTTCATCCCCACAGCGTTGGCCGAG 2174  
1320 GGCCTCAGCTGCTGATGTGCTGATGTAAAGATCTTACTGCTTCCAAACAAATCTC 1379  
Db GGCCTCAGCTGCTGATGTGCTGATGTAAAGATCTTACTGCTTCCAAACAAATCTC 2234  
1380 AGTTGTTTGTCTCAATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACCAAG 1439  
Db AGTTGTTTGTCTCAATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACCAAG 2294  
1440 GCACCAAGGAGTCAATCAAAAGCACTGC 1470  
Db GCACCAAGGAGTCAATCAAAAGCACTGC 2325

## RESULT 4

US-09-040-220D-1  
; Sequence 1, Application US/09040220D  
; Patent No. 6391311  
; GENERAL INFORMATION:  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION  
; FILE REFERENCE: P1122  
; CURRENT APPLICATION NUMBER: US/09/040,220D  
; CURRENT FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Human  
; LOCATION: 2689  
; OTHER INFORMATION: N is A, T, C or G  
US-09-040-220D-1

Query Match 62.0%; Score 914.2; DB 4; Length 2825;  
Best Local Similarity 83.5%; Pred. No. 1.2e-270;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATCGGGATTATGTGGAACATA 61  
Db 61 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAACATA 120  
QY 62 CCCTCGATTCTCTGCTGCCAGAGCGCGCCAGCGCTTCCACCGCAGCGCAGCTTTTCCC 121  
Db 121 CCCTCGATTCTCTGCTGCCAGAGCAGGCTCGCGCTTCCACCGCAGCTTCCCGC 180  
QY 122 CGG---GCTGGGCTGAGCCTTGGAGTGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCC 177  
Db 181 TGGCGGTGGTGAAGAGAGACTCGGGAGTGTCTGCTTCCAAAGTCCCGCGCTGAGTGAGCT 240  
QY 178 CTGCCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCGCTGGCC 237  
Db 241 CTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTGACATCTGCGCTGGCC 300  
QY 238 GGCCAAAGAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGC 297  
Db 301 GGCCAGACACAGGGGACTCAGCGGAATCCAACTGAGTAGTAAATTCAGATTTTCCAGC 360  
QY 298 GACAAAGAACAGAACGAGTGCAGATCCCGGCGCATGAGAGATTGCTACTATATCTGGT 357  
Db 361 AACAAAGAACAGAACGAGTGCAGATCCCGGCGCATGAGAGATTATTAATCTGCTACT 420  
QY 358 AATGGAGCATCCACAGCCGGAAGTTTCTCTACATACCTACCCAGAAATATGGTGGTG 417  
Db 421 AATGGAAGTATTCACAGCCCAAGTTTCTCTACATCTATTCACAGAAATACGGTCTGGTA 480  
QY 418 TGAGATTATGTGCTAGTGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATT 477  
Db 481 TGGAGATTATGTGCTAGTGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATT 540  
QY 478 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCC 537  
Db 541 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGGAGCC 600  
QY 538 AGTGTAGGAAGTGTTTTAGGACGCTGCTGTGGTCTCTGGGACTGTGCCAGGAAAGCAGACT 597  
Db 601 AGTGTAGGAAGTATATTTAGGGCTGCTGTGGTCTCTGGTACTGTACCAAGGAAACAGATT 660  
QY 598 TCTAAAGGAAATCATATCAGGATTAAGATTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 661 TCTAAAGGAAATCAAATTTAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCA 720  
QY 658 GGATTTCTGATCCACTACAGTATTATATGCCCAAGTACAGAAACCAAGCTCTCTCG 717  
Db 721 GGGTCTGATCCACTACCAATTTGTATGCCCAATTTCAAGAGCTGTGAGTCTCTCA 780  
QY 718 GTGTGCCCTCTCATCTTTGTCTATTTGGACCTGCTCAACAACTGCTGTGACTGCTTCAGT 777  
Db 781 GTGCTACCCCTTCAGCTTTGCACTGGACCTGCTTAAATGCTATATACTGCTTTAGT 840  
QY 778 ACCTTGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAGCTTGGACGC 837  
Db 841 ACCTTGAAGAGCTTATTCGATATCTTGAACACAGAGATGGCAGTTGGACTTAGAGAT 900  
QY 838 CTCTACAGCCAACTGAGGAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAA 897  
Db 901 CTATATAGGCCAACTTGGCAAGCTTCTTGGCAAGGCTTTTGTGTTTGGAGAAAAATCCAGA 960

Qy	898	GTGGTGAATCTGAATCTCTCAAGGAAAGGTAAACTCTACAGCTGCACACCCCGAAC	957
Db	961	GTGGTGAATCTGAACCTTTCAACAGAGGAGTAAATATACAGCTGCACACCTCTGTAAC	1020
Qy	958	TTCTCAGTGTCCATACGGGAAAGACTAAAGAGGACAGATACCATATTTCTGGCCAGTTGT	1017
Db	1021	TTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGTTGT	1080
Qy	1018	CTCCTGTCTCAAGCGCTGTGGAGGAAATGTGCCTGTGTCTCCATATTCGAATGAATGT	1077
Db	1081	CTCCTGTGTTAAACGCTGTGTGGGAACTGTGCCTGTGTCTCCAAATTCGAATGAATGT	1140
Qy	1078	CAGTGTGTCCACGCATAAAGTTACAAAAAAGTACCATAGGTCTCTTCAGTTGAGACCACAAA	1137
Db	1141	CAATGTGTCCCAACCAAAAGTTACTAAAAAATACCACGAGGTCTCTTCAGTTGAGACCACAAAG	1200
Qy	1138	ACTGGAGTCAAGGATGTCATAAGTCACTCACTGATGTGGCTCTGGACACACCGAGGAA	1197
Db	1201	ACCGGTGTCAAGGGATGTGCAAAATCACTACCGAGCTGGGCCCTTGGAGCACCATGAGGAG	1260
Qy	1198	TGTCACTGTGTGTGTAGAGGAAACCGCAGGAGGGTAACCTGCAGCCCTTCGTAGCAGCAC	1254
Db	1261	TTCTCACTGTGTGTCTCAGAGGAGCACAGAGGATAGCGCATCACCCACGACGCTC	1317

## RESULT 5

```

RES001_3
US-09-265-686-1
; Sequence 1, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: Fl122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIORITY APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Unknown
; LOCATION: 2689
; OTHER INFORMATION: Any nucleotide
US-09-265-686-1

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Query Match	62.0%;	Score	914.2;	DB	4;	Length	2825;
Best Local Similarity	83.5%;	Pred. No.	1.2e-270;				
Matches 1050;	Conservative	0;	Mismatches	203;	Indels	4;	Gaps
Qy	2	ACCTGGAGACACAGAGAGGCGCTCTAGGAAAAATTTTGGATGGGGATTATGTGGAAACTA	61				
Db	61	AACCTGGAGACACAGAGAGGCGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAAACTA	120				
Qy	62	CCCTGGCGAATCTGTGCTCCAGAGCCGGCCAGCGCGCTTCCACCGGAGCGACGCTTTGCC	121				
Db	121	CCCTGGCGAATCTGTGCTCCAGAGCAGCGCTCGGGCGCTTCCACCCAGTCGACGCTTCGCC	180				
Qy	122	CGG----CGTGGGCTGAGCGCTTGTGAGTGGTGGCTTCCCGAGTGC CGCGCGGAGTGAGCC	177				
Db	181	TGGCGGTGTTGAAGAGACTCGGGAGTCGTGCTTCCAAAGTGCCCGCGGTGAGTGAGCT	240				
Qy	178	CTCGGCCGAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCCCTGCTGACATCTGCGCTGACC	237				
Db	241	CTCACCCGAGTCAGCCAAATGAGCCTCTTTCGGGCTTCTCTCTGCTGACATCTGCGCTGACC	300				
Qy	238	GGCCAAAGACGGGAGCTCGGGCTGAGTCCAACTCGACGACGACAGTTCGAGCTCTCCAGC	297				

```
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-564-595D-32

Query Match      59.6%; Score 878.8; DB 4; Length 1760;
Best Local Similarity 83.4%; Pred. No. 6.9e-260;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGGAACTACCTCGGATCTCTGTCGCCAGAGCGGCTTCACCGC 106
Db |||||
QY 1 ATATGTGGAACTACCTCGGATCTCTGTCGCCAGAGCGGCTTCACCGC 60
Db |||||
QY 107 AGCGCAGCGCTTCCCGCGG---GCTGGGCTGAGCGCTTGGAGTCTGCTCCCGCAGTGCC 162
Db |||||
QY 61 AGTGAGCGCTTCCCGCGGCTGGGAGTCTGGAAGAGTCTGGGAGTCTGCTTCCAAAGTGCC 120
Db |||||
QY 163 CGCGCGAGTGAGCGCTCGCCCGAGTCCAGCCAAATGCTCTCTCGGCTCTCTCTGCTG 222
Db |||||
QY 121 CGCGGTGAGTGAGTCTCAGCCCGAGTCTGTCGCCAGAGCGGCTCGGCGCTTCACCGCC 180
Db |||||
QY 223 ACATGCTCCCTGGCGGCCAAGAGACGGGAGTCTGGGCTGAGTCTCAACTGAGCAGCAG 282
Db |||||
QY 181 ACATGCTCCCTGGCGGCCAAGAGACGGGAGTCTGAGGCGGAATCCAACTGAGTAGTAAA 240
Db |||||
QY 283 TTGCACTCTCCAGCGGCAAGGAACAGACGAGTCTGAGATCCCGCGGCTCAGAGAGT 342
Db |||||
QY 241 TTCCAGTTTCCAGCAACAGGAACAGACGAGTCTGAGATCTCCTCAGCATGAGAGAT 300
Db |||||
QY 343 GTCATCTATCTGTTAATGGAGCATCCAGCCCGAAGTTTCTCTCATACGTACCCAGA 402
Db |||||
QY 301 ATTACTGTCTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCTCATACTTATCCAAGA 360
Db |||||
QY 403 AATATGGTCTGGTGTGAGATTTAGTTGAGTAGATGAAATGTGCGGATCCAGCTGACA 462
Db |||||
QY 361 AATAGCTTCTGGTATGAGATTAGTAGAGTAGAGGAAATGTATGAGTACAACTTAG 420
Db |||||
QY 463 TTTGATGAGATTTGGGTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGT 522
Db |||||
QY 421 TTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGT 480
Db |||||
QY 523 GAAGTTGAGGACCCAGTGTGAGTGTGTTTAGACGCTGTGTGTTCTGGGACTGTG 582
Db |||||
QY 481 GAAGTTGAGGACCCAGTGTGAGTGTGTTTAGGCGCTGTGTGTTCTGGTACTGT 540
Db |||||
QY 583 CCAGGAAGCAGACTTCTAAGGAATCATATCAGGATAAGATTTGTATCTCATGATAT 642
Db |||||
QY 541 CCAGGAAGCAGACTTCTAAGGAATCATATGAGTATGATTTGTATCTCATGATAT 600
Db |||||
QY 643 TTTCCATCTGAACCCGAGTTTGTGATCCACTACAGTATTTATCATGCCAAGTACAGAA 702
Db |||||
QY 601 TTTCTCTTGAACCCAGGTTTGTGATCCACTACAGTATTTATCATGCCAAGTACAGAA 660
Db |||||
QY 703 ACCAGAGTCTTCCGTTGTGCCCCCTTCATCTTTGTCTATTGGACCTGCTCAACATGCT 762
Db |||||

661 GCTGTGAGTCTCTCAGTGTCTACCCCTTCAGCTTTGCCACTGACCTGCTGTAATAGCT 1720
QY 763 GTGACTGCTTTCAGTACCTTTGGAAGAGTGTATTCGGTACCTTAGAGCCAGATGATGGCAG 822
Db 721 ATAAGTCTTTCAGTACCTTTGGAAGAGTGTATTCGGTACCTTAGAGCCAGATGATGGCAG 780
QY 823 GTGACTTTCAGTACCTTTGGAAGAGTGTATTCGGTACCTTAGAGCCAGATGATGGCAG 882
Db 781 TTGACTTTCAGTACCTTTGGAAGAGTGTATTCGGTACCTTAGAGCCAGATGATGGCAG 840
QY 883 GGGAAAAAAGCAAAAGTGTGATCTGAATCTCTCAAGGAAGAGTAAACTTACAGC 942
Db 841 GGAAGAAAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAGATTATACAGC 900
QY 943 TGCACACCCCGGAAGTCTCAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATA 1002
Db 901 TGCACACCTCGTAAGTCTCAGTGTCCATACGGGAGAGAACTAAAGAGAACCATACCAT 960
QY 1003 TTCTGCCAGGTTGCTCTCTCAAGCGCTGTGAGGAAATTTGTCCTGTTGCTCTCCAT 1062
Db 961 TTCTGCCAGGTTGCTCTCTCAAGCGCTGTGAGGAAATTTGTCCTGTTGCTCTCCAT 1020
QY 1063 AATTCAATGAATGTCAGTGTCTCCAGTAAAGTTACAAAAAGTACCATGAGTCTCT 1122
Db 1021 AATTCAATGAATGTCAGTGTCTCCAGTAAAGTTACAAAAAGTACCATGAGTCTCT 1080
QY 1123 CAGTTGAGACCAAAAGTGTGAGTGTGAGGAAATTTGTCCTGTTGCTCTCCAT 1182
Db 1081 CAGTTGAGACCAAAAGTGTGAGTGTGAGGAAATTTGTCCTGTTGCTCTCCAT 1140
QY 1183 GAACACCAAGAGAAATGTCAGTGTCTGAGGAAATTTGTCCTGTTGCTCTCCAT 1242
Db 1141 GAGCACCATGAGGAGTGTGAGTGTGAGGAAATTTGTCCTGTTGCTCTCCAT 1200
QY 1243 TCGTAGCAGCAC 1254
Db 1201 CACCAGCAGCTC 1212

RESULT 7
US-09-706-968-1
; Sequence 1, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60CI
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-706-968-1

Query Match      59.6%; Score 878.8; DB 4; Length 1760;
Best Local Similarity 83.4%; Pred. No. 6.9e-260;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;
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QY 47 ATTATGTGAAACTACCTCTGCGATTCTCTGTGCGCAGAGCCGCGCAGGCGCTTCCACCGC 106
Db 1 ATTATGTGAAACTACCTCTGCGATTCTCTGTGCGCAGAGCAGGCTCGGCGCTTCCACCCC 60
QY 107 AGCGCAGCCTTTCGCCGG-----GCTGGGCTGAGCCTTGGAGTCGTCGCTTCCCGAGTGC 162
Db 61 AGTGACGCTTCCCTTGGCGTGGTGAAGAGACTCGGGAGTCGCTGCTTCCAAAGTGC 120
QY 163 CGCCGCGAGTGAGCCTCGCCCCAGTCAGCCAAATGCTCCTCCTCGGCCCTCCTCTGCTG 222
Db 121 CGCGGTGAGTGAGCTCTCACCCAGCTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTG 180
QY 223 ACATCTGCCCTGGCGGCCAAAGACGGGACTCGGCTGAGTCGACCTGAGTCGACGACAG 282
Db 181 ACATCTGCCCTGGCGGCCAGAGACGGGACTCAGCGGGAATCCAACTGAGTAGTAA 240
QY 283 TTGCAGCTCTCAGCGCAAGAAACAGAACGAGTGCAAGATCCCGGCGATGAGAGTT 342
Db 241 TTCCAGTTTCCAGCAACAAAGAAACAGAACCGAGTACAAAGTCTTCAGCATGAGAA 300
QY 343 GTCACTATATCTGTAATGGGAGCATCCACGCCGGAAGTTTCTCATACGTACCCAGA 402
Db 301 ATTACTGTGCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCTCATACTTATCCAGA 360
QY 403 AATATGGTCTGGTGTGGAGATTAGTTGAGTAGATAAAATGTGCGGATCCAGCTGACA 462
Db 361 AATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTAC 420
QY 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAACGAGATATATGCAAGTATGATTTGTA 522
Db 421 TTTGATGAAGATTGGGCTTGAAGACCGAGATGACATATGCAAGTATGATTTGTA 480
QY 523 GAAGTTGAGGACCCAGTGATGGAAGTGTTTAGGACGCTGTGTGGTCTCGGACTGTG 582
Db 481 GAAGTTGAGAACCCAGTGATGGAACATAATATAGGCGCTGTGTGGTCTCGTACTGTA 540
QY 583 CCAGGAAGCAGACTCTTAAGGAATCATATCAGATAAGATTGTTGATCTGATGATAT 642
Db 541 CCAGGAACACAGATTCTTAAGGAATCAATATAGGATAAGATTGTTGATCTGATGAAT 600
QY 643 TTTTCATCTGAACCCGAGTTCTGCTCCACTACAGTATTATCATGCCACAAAGTCACAGA 702
Db 601 TTTCTCTGACACAGGTTCTGCTCCACTACACATTTGTATGCCAATATTCACAGAA 560
QY 703 ACCAGAGTCTTCGGTGTGCCCCCTTCATCTTTGTCAATGGAACCTGCTCAACAATGCT 762
Db 661 GCTGTGAGTCTTCAGTGTGACCCCCCTTCAGCTTTGCCACTGACCTGCTTAATAATGCT 720
QY 763 GTGACTGCTTCAGTACCTTGAAGAGCTGATTCGTTACCTAGAGCCAGATCGATGGCAG 822
Db 721 ATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGATGGCAG 780
QY 823 GTGGACTTGGACAGCCTCTACAAGCCCAACATGGCAGCTTTTGGCAAGGCTTTCTGTAT 882
Db 781 TTGGACTTGAAGACTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTTTTT 840
QY 883 GGGAAAAAAGCAAGTGTGTAATCTGAATCTCTCAAGGAAGAGTAAATCTCTACAGC 942
Db 841 GGAAGAAAAATCCAGAGTGTGTGATCTGAACCTTCTAAACAGAGAGGTAAGATTATACAG 900
QY 943 TGCACACCCGGAACTTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATA 1002
Db 901 TGCACACCTCGTAATCTTCTCAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACCA 960
QY 1003 TTTGCGCCAGGTTGTCTCTGCTCAAGCGCTGTGGAGGAAATTTGTGCTGTTGTCTCCAT 1062
Db 961 TTTGCGCCAGGTTGTCTCTGCTTAAACGCTGTGTGGGAACTGTGCTGTTGTCTCCAC 1020
QY 1063 AATTGCAATGAATGTCAGTGTCTCCACGTAAGTTTACAAAAAGTACATCAGGTCCTT 1122
Db 1021 AATTGCAATGAATGTCAGTGTCTCCACGTAAGTTTACTAAAAAATACCACGAGTCTT 1080
QY 1123 CAGTTGAGACCAAAACCTGAGCTCAAGGATTGTCATAGTCACTCACTGATGTGGCTGTG 1182
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Db 1081 CAGTTGAGACCAAAAGACCGGTGTGAGGGGATTGCAAAATCACTCACCGACGTGGCCCTG 1140
QY 1183 GAACACCAAGAGGAATGTGACTGTGTGTAGAGGAAAACGAGAGGGGTAACTGACGCT 1242
Db 1141 GAGCACCATGAGAGGTGTGACTGTGTGTGCAAGAGGAGCACAGGAGATAGCCGCATCAC 1200
QY 1243 TCGTAGCAGCAC 1254
Db 1201 CACCAGCAGCTC 1212

RESULT 8
US-09-457-066-1
; Sequence 1, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-457-066-1

Query Match 59.6%; Score 878.8; DB 4; Length 1764;
Best Local Similarity 83.4%; Pred. No. 6.9e-260;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGAAACTACCTCTGCGATTCTCTGTGCGCAGAGCCGCGCAGGCGCTTCCACCGC 106
Db 1 ATTATGTGAAACTACCTCTGCGATTCTCTGTGCGCAGAGCAGGCTCGGCGCTTCCACCCC 60
QY 107 AGCGCAGCCTTTCGCCGG-----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTGC 162
Db 61 AGTGACGCTTCCCTTGGCGTGGTGAAGAGACTCGGGAGTGTGCTTCCAAAGTGC 120
QY 163 CGCCGCGAGTGAGCCTCGCCCCAGTCAGCCAAATGCTCCTCCTCGGCCCTCCTCTGCTG 222
Db 121 CGCGGTGAGTGAGCTCTCACCCAGCTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTG 180
QY 223 ACATCTGCCCTGGCGGCCAAAGACGGGACTCGGCGTGTGAGTCTCAACCTGAGCAGCAAG 282
Db 181 ACATCTGCCCTGGCGGCCAGAGACGGGACTCAGCGGGAATCCAACTGAGTAGTAA 240
QY 283 TTGCAGCTCTCAGCGCAAGAAACAGAACGAGTGCAAGATCCCGGCGATGAGAGTT 342
Db 241 TTCCAGTTTCCAGCAACAAAGAAACAGAACCGAGTACAAAGTCTTCAGCATGAGAA 300
QY 343 GTCACTATATCTGTAATGGGAGCATCCACGCCGGAAGTTTCTCATACGTACCCAGA 402
Db 301 ATTACTGTGCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCTCATACTTATCCAGA 360
QY 403 AATATGGTCTGGTGTGGAGATTAGTTGAGTAGATAAAATGTGCGGATCCAGCTGACA 462
Db 361 AATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTAC 420
QY 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAACGAGATATATGCAAGTATGATTTGTA 522
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Db	421	TTTTGATGAAGAATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTA	480
Qy	523	GAAGTTGAGGAGCCCACTGATGGAAGTGTCTTTAGACGCTGGTGTGGTCTCTGGCACTGTG	582
Db	481	GAAGTTGAGGAACCCAGTGATGGAACATATATAGGGCGCTGGTGTGGTCTTGACTGTA	540
Qy	583	CCAGGAAGCGAGACTTCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGTAGTAT	642
Db	541	CCAGGAAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATGAATAT	600
Qy	643	TTTCCATCTGAACCCGGATCTCGCATCCACTACAGTATTATCATGCCACAGTACAGAA	702
Db	601	TTTCCCTCTGAACCAAGGCTTCGTGATCCACTACAACTGTGTCATGCCACAAATTCAGAA	660
Qy	703	ACCAGAGTCCCTCGGTGTGGCCCCCTTCATCTTTGTTCATTGGACCTGCTCAACAATGCT	762
Db	661	GCTGTAGTCCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCT	720
Qy	763	GTGACTGCCCTTCAGTACTCTTGGAAAGAGCTGATTCGGTACTTAGAGCCAGATTCGATGGCAG	822
Db	721	ATAACTGCCCTTTAGTACTCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGATGGCAG	780
Qy	823	GTGACTTGGACAGCCTCTCAAGCCCAACATGGCAGCTTTTGGCGCAGGCTTCCCTGTAT	882
Db	781	TTGACTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTT	840
Qy	883	GGGAAAAAAGCAAGTGGTGAATCTGHAATCTCTCAAGGAAGAGGTAAAACTCTACAGC	942
Db	841	GGAAGAAAAATCCAGAGTGGTGGATCTGAAACCTTCTAACAGAGGAGGTAAGATTTATACAGC	900
Qy	943	TGCACACCCGGAACTTCTCAGTGTCCATACGGGAAGAGCTTAAGAGAGACAGATACCATA	1002
Db	901	TGCACACCTCGTAACTTCTCAGTGTCCATTAAGGGAAGAACTTAAAGAGAAACCGATACCATT	960
Qy	1003	TTCTGGCCAGGTTGCTCCTCGGTCAAGCGCTGTGCGAGAAATCTGCCTGTGTGCTCCAT	1062
Db	961	TTCTGGCCAGGTTGCTCCTCGGTAAAGCTGTGGTGGAACTGTGCTGTGTCTCCAC	1020
Qy	1063	AAATTGCAATGAATGTCAGTGTGCCACGTAAAGTTACAAAAAGTACCATGAGTCCCTT	1122
Db	1021	AAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCACGAGTCCCTT	1080
Qy	1123	CAGTTGAGACCAAAACTGGAGTCAAGGGATTCGATAAGTCACTCATGTGATGGGCTGTG	1182
Db	1081	CAGTTGAGACCAAGACCGGTGTGAGGGGATTCGACAAATCACTCAACCGACGTGGCCCTG	1140
Qy	1183	GAAACACCAAGGAATGTGACTGTGTGTGTAGAGGAAACGACGAGAGGTAACCTGCAGCCT	1242
Db	1141	GAGCACCATGAGGAGTGTGACTGTGTGTGTGACAGGGAGCAAGAGAGATAGCCGCATCAC	1200
Qy	1243	TCGTAGCAGCAC	1254
Db	1201	CACCAGCAGCTC	1212

## RESULT 9

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1  US-09/457-066-50
2  /
3  / Sequence 50, Application US/09457066
4  / Patent No. 6432673
5  /
6  / GENERAL INFORMATION:
7  /
8  / APPLICANT: Gao, Zeren
9  /
10 / APPLICANT: Hart, Charles E.
11 /
12 / APPLICANT: Piddington, Christopher S.
13 /
14 / APPLICANT: Sheppard, Paul O.
15 /
16 / APPLICANT: Shoemaker, Kimberly E.
17 /
18 / APPLICANT: Gilbertson, Debra G.
19 /
20 / APPLICANT: West, James W.
21 /
22 / TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
23 /
24 / FILE REFERENCE: 98-60
25 /
26 / CURRENT APPLICATION NUMBER: US/09/457,066
27 /
28 / CURRENT FILING DATE: 1999-12-07
29 /
30 / NUMBER OF SEQ ID NOS: 50
31 /
32 / SOFTWARE: FASTSEQ for Windows Version 3.0
33 /

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Db      980 AGACCGGTGTGAGGAGTTCACAAATCACTACCGAGCTGGCCCTGGAGCACCATGAGG 1039
QY      1196 AATGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232
Db      1040 AGTGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076

RESULT 10
US-09-706-968-50
; Sequence 50, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fused DNA
US-09-706-968-50

Query Match      50.6%; Score 745.8; DB 4; Length 1095;
Best Local Similarity 84.3%; Pred. No. 4e-219;
Matches 840; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY      236 CCGGCCCAAGAAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAGAGTTGCGACTCTCCA 295
Db      80 CCGGCCAGAGACAGGGGACTCAGCGGGAATCCAACTGAGTAGTAATCCAGTTTCCA 139
QY      296 GCGACAAGGAACAGAACGGAGTGCAGATCCCGGCGATGAGAGAGTTGTCACATATCTG 355
Db      140 GCAACAAGGAACAGAACGGAGTGCAGATCCCGGCGATGAGAGAGTTATTAATCTGTCTA 199
QY      356 GTAAATGGCAGATCCACAGCCCGAAAGTTTCTCATAGTACCACCAAGAAATATGGTGTGG 415
Db      200 CTAAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAGAAATACGGTCTGG 259
QY      416 TGTGGAGATTAGTTGCGAGTAGATGAAATGTGGCGATCCAGCTGACATTTGATGAGAGAT 475
Db      260 TATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAACTTACGTTTGTATGAAAGAT 319
QY      476 TTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGATTGAGAGC 535
Db      320 TTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAGATTGAGAGAC 379
QY      536 CCAGTGTAGGAAGTGTGTTTGTAGGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAACGAGA 595
Db      380 CCAGTGTAGGAAGTGTGTTTGTAGGACGCTGGTGTGTTCTGGTACTGTACCAAGGAAACAGA 439
QY      596 CTTCTAAGGAATCATATCAGGTAAGATTTGTATCTGTGATGAGTATTTTCCATCTGAAC 655
Db      440 TTTCTAAGGAATCAATATAGGATAAGATTTGTATCTGTGATGATATTTTCTCTCTGAAC 499
QY      656 CCGGATTCGATCCACTACAGTATATATCATGCCACCAAGTACAGAAACACGAGTCCCT 715
Db      500 CAGGTTCTGATCCACTACAGTATATATCATGCCACCAATTCACAGAGCTGTGAGTCCCT 559
QY      716 CCGTGTGGCCCTTCTATTTTGTATGAGACCTGCTCAACAAATGCTGTGACTGCCTTCA 775

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Db      560 CAGTGTACCCCTTACGTTTGGCTTGGCACTTGTCTTAAATAGCTATAATGCTCTTAA 619
QY      776 GTACCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGGACTTGGACA 835
Db      620 GTACCTTGGAGAGCTTATTCGATATCTTGAACAGAGAGATGGAGTGTGAGCTTAGAG 679
QY      836 GCCTCTACAAGCCAAACATGGCAGCTTTTGGGCAAGGCTTTTCTGTATGGGAAAAAAGCA 895
Db      680 ATCTATATAGGCCAACTTGGCACTTCTTGGCAAGGCTTTTGTGGAAGAAAAATCCA 739
QY      896 AAGTGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGGACACCCCGGA 955
Db      740 GAGTGTGGATCTGAACCTTCTAAACAGAGGAGGTAAAGATTATACAGCTGACACCTCGTA 799
QY      956 ACTTCTCAGTGTCCATACGGGAAGAGCTTAAAGAGACAGATACCATATTTCTGGCCAGTT 1015
Db      800 ACTTCTCAGTGTCCATAGGAGGAGACTAAAGAGACCGATACCATTTTCTGGCCAGTT 859
QY      1016 GTCTCTCGTCAAGCGCTGTGGAGAAATTTGTGCTGTGTCTTCCATATTTGCAATGAAT 1075
Db      860 GTCTCTCGTAAACCGCTGTGTGGGAACCTGTGCTGTGTGTCTCCACAAATGCAATGAAT 919
QY      1076 GTCACTGTCTCCAGTAAAGTTTACAAAAGAGTACCATGAGTCTCTTCAGTTGAGACCA 1135
Db      920 GTCAATGTGTCCCAAGCAAGTACTAAAAGTACCAGAGTCTCTTCAGTTGAGACCA 979
QY      1136 AAACGTGAGTCAAGGGAATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACACGAGG 1195
Db      980 AGACCGGTGTGAGGAGATTGCACAAATCACTCAGCAGTGGCCCTGGAGCACCATGAGG 1039
QY      1196 AATGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1232
Db      1040 AGTGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1076

RESULT 11
US-09-457-066-6
; Sequence 6, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
; OTHER INFORMATION: 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match      44.8%; Score 660.8; DB 4; Length 1035;
Best Local Similarity 52.9%; Pred. No. 5.4e-193;
Matches 547; Conservative 250; Mismatches 237; Indels 0; Gaps 0;

QY      196 ATGCTCTCTCTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 255

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; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
; US-09-540-224-3

Query Match      9.3%; Score 137.2; DB 4; Length 1472;
Best Local Similarity 52.5%; Pred. No. 6.7e-32;
Matches 496; Conservative 0; Mismatches 373; Indels 75; Gaps 6;

356 GTAATGGAGATCCACAGCCCGAAGTTTCTCATAGTACCCAGAAATATGGTCTGG 415
Db |||||
416 TGTGGAGATTAGTTCAGTAGATCAAAATGTGCGGATCCAGCTGACATTTGATGAGAT 475
Db |||||
331 CATGGTGGCTCGGTTCC---CCAGGAGAAACACGGATACAACTGTCTTGCACATCAAT 387
Db |||||
476 TTGGGCTGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGAGC 535
Db |||||
388 TCGGACTAGAGAACGAGAAATGACATTTGTAGTATGACTTTGTGGAAGTTGAAGAAG 447
Db |||||
536 CCAGTGATGGGAAG-----TGTTTATGAGACGCTGTGTGGTTCTGGGACTGTGCCAGGA 589
Db |||||
448 TCTCAGAGAGCAGCACTGTGTGTCAGAGGAGATGTGTGGCCACAGGAGATCCCTCCAA 507
Db |||||
590 ACAGACTCTTAAAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCAT 649
Db |||||
508 GGATAACGTCAGAGAACAAACAGATTAATAATGCTGATGACTACTTTGTGG 567
Db |||||
650 CTGACCCCGGATTCGCTATCCACTACAGTATAT-----CATGCCACAAGTCA 697
Db |||||
568 CAAAACCTGGATTCAAGATTTATTATTCATTTGTGGGAGATTTCACACCGAGCGCT 627
Db |||||
698 CAGAACCCACAGAGTCTTTCGGTGTGCGCCCTTCATCTTTGTCTATGGAACCTG 750
Db |||||
628 CAGAGACCAACTGGGAATCAGTACAAGCTCTTTCTCTGGGGTGTCTTACTCTCCAT 687
Db |||||
751 -----CTCAACAATGCTGTGACTGCGCTTCAGTA 778
Db |||||
688 CAATAACGGACCCCACTCTCACTGCTGATGCTCTGGACAAAACCTGTCGAGAATTGGATA 747
Db |||||
779 CCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTCGACAGCC 838
Db |||||
748 CCGTGGAGATCTACTTAAGCACTTCAATCAGTGTCTTGGCAGATGATCTGGAGATT 807
Db |||||
839 TCTACAGCCCAACATGCGAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAAG 898
Db |||||
808 TGTATCTGGACACCCCTCATTTATAGAGCGAGGTATACCATGATCGGAAATCCA----- 861
Db |||||
899 TGGTGAATCTGAATCTCTCAGAGAGAGGTAAACTCTACAGCTGACACACCCCGAAT 958
Db |||||
862 AAGTGGACCTGGACAGGCTCAATGATGATCAAGCGTTTACAGTTGCACTCCCGAGAAATC 921
Db |||||
959 TCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATTTCTGGCCAGGTTGTC 1018
Db |||||
922 ACTCTGTGAACCTCAGGGAGAGCTGAAGCTGACCAATGAGCTTCTTCCAGATGCC 981
Db |||||
1019 TCCTGGTCAAGCGCTGTGGAGAAATTTGTGCTGCTTCTCCATAATGCAATGAATGTC 1078
Db |||||
982 TCCTCGTGCAGCGTGTGGTGGCACTGTGTTGTCGGAACTGTCAACTGGAAGTCTCTGCA 1041
Db |||||

RESULT 15
US-09-564-595D-52
; Sequence 52, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
; US-09-564-595D-52

Query Match      9.3%; Score 137.2; DB 4; Length 1472;
Best Local Similarity 52.5%; Pred. No. 6.7e-32;
Matches 496; Conservative 0; Mismatches 373; Indels 75; Gaps 6;

356 GTAATGGAGATCCACAGCCCGAAGTTTCTCATAGTACCCAGAAATATGGTCTGG 415
Db |||||
271 GCAATGGCCATGTGCGAGTCTCTCGCTTCCCGAAGCAGTACCCAGGAACTCTTCTGA 330
Db |||||
416 TGTGGAGATTAGTTCAGTAGATCAAAATGTGCGGATCCAGCTGACATTTGATGAGAT 475
Db |||||
331 CATGGTGGCTCGGTTCC---CCAGGAGAAACACGGATACAACTGTCTTGCACATCAAT 387
Db |||||
476 TTGGGCTGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGAGC 535
Db |||||
388 TCGGACTAGAGAACGAGAAATGACATTTGTAGTATGACTTTGTGGAAGTTGAAGAAG 447
Db |||||
536 CCAGTGATGGGAAG-----TGTTTATGAGACGCTGTGTGGTTCTGGGACTGTGCCAGGA 589
Db |||||
448 TCTCAGAGAGCAGCACTGTGTGTCAGAGGAGATGTGTGGCCACAGGAGATCCCTCCAA 507
Db |||||
590 ACAGACTCTTAAAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCAT 649
Db |||||
508 GGATAACGTCAGAGAACAAACAGATTAATAATGCTGATGACTACTTTGTGG 567
Db |||||
650 CTGACCCCGGATTCGCTATCCACTACAGTATAT-----CATGCCACAAGTCA 697
Db |||||
568 CAAAACCTGGATTCAAGATTTATTATTCATTTGTGGGAGATTTCACACCGAGCGCT 627
Db |||||
698 CAGAACCCACAGAGTCTTTCGGTGTGCGCCCTTCATCTTTGTCTATGGAACCTG 750
Db |||||
628 CAGAGACCAACTGGGAATCAGTACAAGCTCTTTCTCTGGGGTGTCTTACTCTCCAT 687
Db |||||
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QY	751	-----CTCAAAATGCTGTGACTGCTTCACTA	778
Db	688	CAATAACGGACCCCACTCTACTGCTGATGCCCTGGACAAAACTGTGCGAATTCGATA	747
QY	779	CCTTGGAAAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCC	838
Db	748	CGTGGAAAGATCTACTTAAGCACCTTCAATCCAGTGTCTTGGCAAGATGATCTGGAGAATT	807
QY	839	TCTACAAGCCCAACATGGCAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAG	898
Db	808	TGTATCTGGACACCCCTCATTTATAGAGCAGGTCTACCATGATCGGAATCCA-----	861
QY	899	TGGTGAATCTGNAATCTCTCAAGGAAGAGGTAATACTCTACAGCTGCACACCCCGAACT	958
Db	862	AAGTGGACCTGGACAGGCTCAATGATGATGTCAAGCGTTACAGTTGCACTCCAGGAATC	921
QY	959	TCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTC	1018
Db	922	ACTCTGTGAACCTCAGGGAGGAGCTGAAGCTGACCAATGCAGTCTTCTTCCCACGATGCC	981
QY	1019	TCCTGGTCAAGCGCTGTGGAGGAATTTGGCCTGTGTCTCCATTAATTGCAATGAATGTC	1078
Db	982	TCCTCGTGCAGCGCTGTGGTGGCAACTGTGTGTGGCAACTGTCAACTGGAAGTCTCTGCA	1041
QY	1079	AGTGTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGTCTTTCAGTTTGAGACC-----	1133
Db	1042	CATGCAGCTCAGGGAGACAGTGAAGAGTATCATGAGGTATTGAAGTTGAGCCTGGAC	1101
QY	1134	-----AAAAACTGGAGTCAAGGATTGCATAAGTCACTCATGATGGCTCTGGAAACCC	1189
Db	1102	ATTTCAAGAGAAGGGCAAGCTAAGAAATATGGCTCTTGTGTATATCCAGCTGGATCATC	1161
QY	1190	ACGAGGAATGTGACTGTGTGTAGAGGAACGCAGGAGGTAA	1233
Db	1162	ATGAGCGATGTGACTGTATCTCAGCTCAAGACCACCTCGATAA	1205

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Job time : 77.0008 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 03:42:52 ; Search time 362.884 Seconds  
(without alignments)  
13382.717 Million cell updates/sec

Title: US-09-852-209A-6

Perfect score: 1474

Sequence: 1 cacttgagacagaagag.....aatcacaagcactgcaccg 1474

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1473	99.9	1474	14	US-10-131-600-6
3	1444.8	98.0	3571	9	US-09-823-033-3
4	1444.8	98.0	3571	13	US-10-139-583-42
5	1444.8	98.0	3571	14	US-10-264-361-3
6	914.2	62.0	2825	14	US-10-178-442-1
7	914.2	62.0	2839	11	US-09-796-753-5
8	914.2	62.0	2849	10	US-09-978-295A-487
9	914.2	62.0	2849	10	US-09-978-697-487
10	914.2	62.0	2849	10	US-09-978-132A-487
11	914.2	62.0	2849	10	US-09-993-832A-487
12	914.2	62.0	2849	11	US-09-978-189-487
13	914.2	62.0	2849	11	US-09-978-608A-487
14	914.2	62.0	2849	11	US-09-978-585A-487
15	914.2	62.0	2849	11	US-09-978-131A-487
16	914.2	62.0	2849	11	US-09-978-403A-487

17 914.2 62.0 2849 11 US-09-978-564A-487 Sequence 487, App  
18 914.2 62.0 2849 11 US-09-999-833A-487 Sequence 487, App  
19 914.2 62.0 2849 11 US-09-981-915A-487 Sequence 487, App  
20 914.2 62.0 2849 11 US-09-978-824-487 Sequence 487, App  
21 914.2 62.0 2849 11 US-09-918-585A-487 Sequence 487, App  
22 914.2 62.0 2849 11 US-09-978-423A-487 Sequence 487, App  
23 914.2 62.0 2849 11 US-09-978-193A-487 Sequence 487, App  
24 914.2 62.0 2849 11 US-09-999-830A-487 Sequence 487, App  
25 914.2 62.0 2849 11 US-09-978-757B-487 Sequence 487, App  
26 914.2 62.0 2849 11 US-09-978-187B-487 Sequence 487, App  
27 914.2 62.0 2849 11 US-09-978-643A-487 Sequence 487, App  
28 914.2 62.0 2849 12 US-09-978-375A-487 Sequence 487, App  
29 914.2 62.0 2849 12 US-09-978-188A-487 Sequence 487, App  
30 914.2 62.0 2849 12 US-09-978-298A-487 Sequence 285, App  
31 914.2 62.0 2849 12 US-10-137-870-285 Sequence 285, App  
32 914.2 62.0 2849 12 US-10-140-018-285 Sequence 285, App  
33 914.2 62.0 2849 12 US-10-140-021-285 Sequence 285, App  
34 914.2 62.0 2849 12 US-10-140-274-285 Sequence 285, App  
35 914.2 62.0 2849 12 US-10-140-471-285 Sequence 285, App  
36 914.2 62.0 2849 12 US-10-140-807-285 Sequence 285, App  
37 914.2 62.0 2849 12 US-10-140-922-285 Sequence 285, App  
38 914.2 62.0 2849 12 US-10-140-924-285 Sequence 285, App  
39 914.2 62.0 2849 12 US-10-140-926-285 Sequence 285, App  
40 914.2 62.0 2849 12 US-10-141-702-285 Sequence 285, App  
41 914.2 62.0 2849 12 US-10-141-704-285 Sequence 285, App  
42 914.2 62.0 2849 12 US-10-142-421-285 Sequence 285, App  
43 914.2 62.0 2849 12 US-10-142-432-285 Sequence 285, App  
44 914.2 62.0 2849 12 US-10-142-767-285 Sequence 285, App  
45 914.2 62.0 2849 12 US-10-142-767-285 Sequence 285, App

#### ALIGNMENTS

#### RESULT 1

US-09-852-209A-6  
; Sequence 6, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: RASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; FILE REFERENCE: THEREFOR, AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t

#### DNA CODING



US-09-852-209A-6

Query Match									
Best Local Similarity 99.9%; Score 1473; DB 10; Length 1474;									
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGAAACT	60						
Db	1	CACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGAAACT	60						
Qy	61	ACCTCGGATTCCTCTGCTGCAGAGCCGCGAGGCGCTTCCACCCGAGCGAGCCTTCC	120						
Db	61	ACCTCGGATTCCTCTGCTGCAGAGCCGCGAGGCGCTTCCACCCGAGCGAGCCTTCC	120						
Qy	121	CGGGCTGGGCTGAGCTTTGGAGTGGTCTCCCGAGTCCCGCGCGAGTGAGCCCTC	180						
Db	121	CGGGCTGGGCTGAGCTTTGGAGTGGTCTCCCGAGTCCCGCGCGAGTGAGCCCTC	180						
Qy	181	GCCGAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTTGGCGGC	240						
Db	181	GCCGAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTTGGCGGC	240						
Qy	241	CAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGAC	300						
Db	241	CAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGAC	300						
Qy	301	AAGGAACGAACGGAGTGAAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAAT	360						
Db	301	AAGGAACGAACGGAGTGAAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAAT	360						
Qy	361	GGGAGATCCAGCGCCGAGTTTCTCATAGTACCCAGAAATATGCTGCTGGTGG	420						
Db	361	GGGAGATCCAGCGCCGAGTTTCTCATAGTACCCAGAAATATGCTGCTGGTGG	420						
Qy	421	AGATTAGTTGAGTGAATGAGATGCGGATCCAGCTGACATTTGATCAGAGATTTGG	480						
Db	421	AGATTAGTTGAGTGAATGAGATGCGGATCCAGCTGACATTTGATCAGAGATTTGG	480						
Qy	481	CTGGAAGTCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCCACT	540						
Db	481	CTGGAAGTCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCCACT	540						
Qy	541	GATGAAGTGTATAGGAGCTGGTGGTCTGGGACTGTGCCAGGAAGCAGACTTCT	600						
Db	541	GATGAAGTGTATAGGAGCTGGTGGTCTGGGACTGTGCCAGGAAGCAGACTTCT	600						
Qy	601	AAAGGAATCATATCAGGATAAGATTTGATCTGATGAGTATTTTCCATCTCAACCCGGA	660						
Db	601	AAAGGAATCATATCAGGATAAGATTTGATCTGATGAGTATTTTCCATCTCAACCCGGA	660						
Qy	661	TTCTGATCCACTACAGTATTAATGATGCAAGTCAAGAAACCAAGAGTCTTGGTG	720						
Db	661	TTCTGATCCACTACAGTATTAATGATGCAAGTCAAGAAACCAAGAGTCTTGGTG	720						
Qy	721	TTGCCCTTCACTTTGTCATGAGCTGTCAACATGCTGACTGCCCTTCAGTACC	780						
Db	721	TTGCCCTTCACTTTGTCATGAGCTGTCAACATGCTGACTGCCCTTCAGTACC	780						
Qy	781	TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACAGCCTC	840						
Db	781	TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACAGCCTC	840						
Qy	841	TACAAGCCACATGCGAGCTTTTGGCAAGCTTTCTCTGATGGGAAAAAGCAAGTG	900						
Db	841	TACAAGCCACATGCGAGCTTTTGGCAAGCTTTCTCTGATGGGAAAAAGCAAGTG	900						
Qy	901	GTGAATCTGAATCTCTCAAGCAAGAGTAAACTCTACAGCTGCACACCCCGAATTC	960						
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Qy	961	TCAGTGTCCATCGGGAAGAGCTAAAGAGGACAGATACCATTCTGGCCAGGTTGTCTC	1020						
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RESULT 2

US-10-131-600-6  
; Sequence 6, Application US/10131600  
; Publication No. US20030082670A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Amica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure

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; LOCATION: (1447)
; OTHER INFORMATION: can be a, c, g or t
US-10-131-600-6

Query Match          99.9%; Score 1473; DB 14; Length 1474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60
Db 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60

QY 61 ACCCTGGATTCTCTGCTGCAGAGCGCGCAGCGCTTCCACCGCAGCGAGCCTTCC 120
Db 61 ACCCTGGATTCTCTGCTGCAGAGCGCGCAGCGCTTCCACCGCAGCGAGCCTTCC 120

QY 121 CCGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCCGCGAGTGGCCCTC 180
Db 121 CCGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCCGCGAGTGGCCCTC 180

QY 181 GCGCCAGTACGCAAAATGCTCTCTCGGCTCTCTCTGCTGCAATCTGCCCTGGCCGGC 240
Db 181 GCGCCAGTACGCAAAATGCTCTCTCGGCTCTCTCTGCTGCAATCTGCCCTGGCCGGC 240

QY 241 CAAAGAACGGGACTCGGGCTGAGTCCCACTGAGCAGAGTTCGACTATCTGTTAAT 300
Db 241 CAAAGAACGGGACTCGGGCTGAGTCCCACTGAGCAGAGTTCGACTATCTGTTAAT 300

QY 301 AAGGAAACAGAACGGAGTGCAGATCCCGGCTGAGAGAGTTCGACTATCTGTTAAT 360
Db 301 AAGGAAACAGAACGGAGTGCAGATCCCGGCTGAGAGAGTTCGACTATCTGTTAAT 360

QY 361 GGGAGCATCCACAGCCGAGTTCCTCCTACGTAACGTAACGTAACGTAACGTAACG 420
Db 361 GGGAGCATCCACAGCCGAGTTCCTCCTACGTAACGTAACGTAACGTAACGTAACG 420

QY 421 AGATTAGTTCAGTAGATGAATATGCGGATCCAGTCCAGTCCAGTCCAGTCCAGT 480
Db 421 AGATTAGTTCAGTAGATGAATATGCGGATCCAGTCCAGTCCAGTCCAGTCCAGT 480

QY 481 CTGGAAGTCCAGAACGATATATGCAAGTATGATTTCTGAGAGTTCAGGAGCCAGT 540
Db 481 CTGGAAGTCCAGAACGATATATGCAAGTATGATTTCTGAGAGTTCAGGAGCCAGT 540

QY 541 GATGGAAGTCTTTAGAACGCTGGTGGTCTGCGGACTCTGCGGACTCTGCGGAAAGCACTTCT 600
Db 541 GATGGAAGTCTTTAGAACGCTGGTGGTCTGCGGACTCTGCGGACTCTGCGGAAAGCACTTCT 600

QY 601 AAAGGAAATCATATCAGATAAGATTTGTATCTGATGAGTATTTCCATCTGACCCGGA 660
Db 601 AAAGGAAATCATATCAGATAAGATTTGTATCTGATGAGTATTTCCATCTGACCCGGA 660

QY 661 TTCTGCATCCACTACAGTATTTATCATGCCCAAGTCAAGATCAAGAACCCAGTCTCTCGGTG 720
Db 661 TTCTGCATCCACTACAGTATTTATCATGCCCAAGTCAAGATCAAGAACCCAGTCTCTCGGTG 720

QY 721 TTGCCCCCTTCATCTTGTATGAGTCTGCTCAAGTCTGATGAGTCTGATGAGTCTGATGAGT 780
Db 721 TTGCCCCCTTCATCTTGTATGAGTCTGCTCAAGTCTGATGAGTCTGATGAGTCTGATGAGT 780

QY 781 TTGGAAGAGTGTATTCGGTACCTAGAGCCAGATCGATGCGAGTGGAGTGGACGCGCTC 840
Db 781 TTGGAAGAGTGTATTCGGTACCTAGAGCCAGATCGATGCGAGTGGAGTGGACGCGCTC 840

QY 841 TACAAGCAACATGGCAGCTTTTGGCAAGGCTTTCTGATGAGGAAAGAAAGCAAGTG 900
Db 841 TACAAGCAACATGGCAGCTTTTGGCAAGGCTTTCTGATGAGGAAAGAAAGCAAGTG 900

QY 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTCTGCAACCCCGGAACTTC 960
Db 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTCTGCAACCCCGGAACTTC 960

QY 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTC 1020
Db 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTC 1020

QY 1021 CTGCTCAAGCGCTGTGGAGAAATTTGCTGTTGTTCTCCATAATTTGCAATGTAATGTCTCAG 1080
Db 1021 CTGCTCAAGCGCTGTGGAGAAATTTGCTGTTGTTCTCCATAATTTGCAATGTAATGTCTCAG 1080

QY 1081 TGTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAACT 1140
Db 1081 TGTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAACT 1140

QY 1141 GGAGTCAAGGATTCATAGTCACTCACTGATGCTCTGGAACACCCAGGAGGATGT 1200
Db 1141 GGAGTCAAGGATTCATAGTCACTCACTGATGCTCTGGAACACCCAGGAGGATGT 1200

QY 1201 GACTGTGTGTAGAGAAACGAGGAGGTAACCTGACGCTTCTGAGCAGCACACGCTGA 1260
Db 1201 GACTGTGTGTAGAGAAACGAGGAGGTAACCTGACGCTTCTGAGCAGCACACGCTGA 1260

QY 1261 GCACTGCAATTCGTGTATCCCGCAAGCAACCTTCACTCCCGCAGCGTTGGCGCAGG 1320
Db 1261 GCACTGCAATTCGTGTATCCCGCAAGCAACCTTCACTCCCGCAGCGTTGGCGCAGG 1320

QY 1321 GCTCTGAGTCTGATGCTGGCTATGTAAGATCTTACTCTGCTCCAAACCAATTTCTCA 1380
Db 1321 GCTCTGAGTCTGATGCTGGCTATGTAAGATCTTACTCTGCTCCAAACCAATTTCTCA 1380

QY 1381 GTTGTGTTCTCAATAGCTTCCCTGCGAGTCTCAAGTCTTCTTAAAGACACAGG 1440
Db 1381 GTTGTGTTCTCAATAGCTTCCCTGCGAGTCTCAAGTCTTCTTAAAGACACAGG 1440

QY 1441 CACCAANAGAGTCAATCAAAAGCACTGCACCG 1474
Db 1441 CACCAANAGAGTCAATCAAAAGCACTGCACCG 1474

RESULT 3
US-09-823-033-3
; Sequence 3, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-823-033-3

Query Match          98.0%; Score 1444.8; DB 9; Length 3571;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACTA 61
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACTA 915

QY 62 CCTGCGATTTCTGCTGCGAGAGCGCGCAGGCTTCCACCGCAGCGAGCCTTTCCC 121
Db 916 CCCTGCGATTTCTGCTGCGAGAGCGCGCAGGCTTCCACCGCAGCGAGCCTTTCCC 975

QY 122 CGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTGGCGCGGAGTGAGCCCTCG 181
Db 122 CGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTGGCGCGGAGTGAGCCCTCG 181
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976 C-GGCTGGGCTGAGCCTTGGAGTCGTGCTCTCCCGAGTGCCTCG 1034  
182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGACATCTCCCTGCGCGCC 241  
1035 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGACATCTCCCTGCGCGCC 1094  
242 AAAGAACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCCAGCGACA 301  
1095 AAAGAACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCCAGCGACA 1154  
302 AGGACAGAACGGAGTCAAGATCCCGGCTGAGAGAGTGTCACTATATCTGGTAATG 361  
1155 AGGACAGAACGGAGTCAAGATCCCGGCTGAGAGAGTGTCACTATATCTGGTAATG 1214  
362 GGAGCATCCACAGCCGAGTTTCTCATAGCTACCCAGAAATATGCTGCTGGTGGGA 421  
1215 GGAGCATCCACAGCCGAGTTTCTCATATACATCCCAAGAAATATGCTGCTGGTGGGA 1274  
422 GATTAGTTGCAGTAGTGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATTGGGC 481  
1275 GATTAGTTGCAGTAGTGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATTGGGC 1334  
482 TGGAGATCCAGAGACATATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 541  
1335 TGGAGATCCAGAGACATATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 1394  
542 ATGGAAGTGTTTTAGGACGCTGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTTCTA 601  
1395 ATGGAAGTGTTTTAGGACGCTGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTTCTA 1454  
602 AAGGAATCATATCAGGATAGATTGTATCTGATGAGTATTTCCATCTGAACCCGAT 661  
1455 AAGGAATCATATCAGGATAGATTGTATCTGATGAGTATTTCCATCTGAACCCGAT 1514  
662 TCTGCATCCATACAGTATATCATGCCACAGTCAAGAAACACAGAGTCTCTCGGCT 721  
1515 TCTGCATCCATACAGTATATCATGCCACAGTCAAGAAACACAGAGTCTCTCGGCT 1574  
722 TGCCCCCTTCACTTTGTCATTGACCTGTCTCAACATGCTGTGACTGCTCTCACTACT 781  
1575 TGCCCCCTTCACTTTGTCATTGACCTGTCTCAACATGCTGTGACTGCTCTCACTACT 1634  
782 TGGAGAGCTGATTCGTTACCTAGGACGAGATCGATGCGAGTGGACTTGGACGCTCT 841  
1635 TGGAGAGCTGATTCGTTACCTAGGACGAGATCGATGCGAGTGGACTTGGACGCTCT 1694  
842 ACAAGCCAACTGCGAGCTTTGGCAAGGCTTCTCTATGGGAAAAAAGCAAGTGG 901  
1695 ACAAGCCAACTGCGAGCTTTGGCAAGGCTTCTCTATGGGAAAAAAGCAAGTGG 1754  
902 TGAATCTGAATCTCTCAAGGAAGGTAAACTCTACAGTGCACACCCCGAACTTCT 961  
1755 TGAATCTGAATCTCTCAAGGAAGGTAAACTCTACAGTGCACACCCCGAACTTCT 1814  
962 CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCCT 1021  
1815 CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCCT 1874  
1022 TGGTCAAGCGCTGTGGAGAAATTTGCTGCTCTCCATAATGCAATGAATGTCAGT 1081  
1875 TGGTCAAGCGCTGTGGAGAAATTTGCTGCTCTCCATAATGCAATGAATGTCAGT 1934  
1082 GTGTCCACGTAAGTTTCAAAAAGTACCATAGGTCCTTCACTGATGAGACCAAAACTG 1141  
1935 GTGTCCACGTAAGTTTCAAAAAGTACCATAGGTCCTTCACTGATGAGACCAAAACTG 1994  
1142 GAGTCAAGGGATTGATAGTCACTCACTGATGAGTCTGGAACACACGAGGATG 1201  
1995 GAGTCAAGGGATTGATAGTCACTCACTGATGAGTCTGGAACACACGAGGATG 2054  
1202 ACTGTGTGTAGAGGAACGAGAGGTTAACTGACGCTTCTGATGAGCAGCAGTGG 1261  
2055 ACTGTGTGTAGAGGAACGAGAGGTTAACTGACGCTTCTGATGAGCAGCAGTGG 2114

1362 CACTGGCATTCTGTGTACCCCAAGCAACTTTCATCCCAAGCGTGTGGCCGAGGG 1321  
2115 CACTGGCATTCTGTGTACCCCAAGCAACTTTCATCCCAAGCGTGTGGCCGAGGG 2174  
1322 CTCTCAGCTGCTGATGCTGTGTAAGATCTTACTCTCCAAACCAAAATCTCAG 1381  
2175 CTCTCAGCTGCTGATGCTGTGTAAGATCTTACTCTCCAAACCAAAATCTCAG 2234  
1382 TTGTTGCTTCAATAGCTTCCCTGCGAGACTTCAAGTGTCTTCTAAAGACCAAGGC 1441  
2235 TTGTTGCTTCAATAGCTTCCCTGCGAGACTTCAAGTGTCTTCTAAAGACCAAGGC 2294  
1442 ACCAAGAGAGTCAATCAAAAGCACTGC 1470  
2295 ACCAAGAGAGTCAATCAAAAGCACTGC 2323

RESULT 4  
US-10-139-583-42  
; Sequence 42, Application US/10139583  
; Publication No. US2002017193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10139,583  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 09/457,066  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-10-139-583-42

Query Match 98.0%; Score 1444.8; DB 13; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 61  
DB 856 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 915  
QY 62 CCCTGCGATTTCTCTGCTGCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCTTTCC 121  
DB 916 CCCTGCGATTTCTCTGCTGCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCTTTCC 975  
QY 122 CGGCTGGCTGAGCTTGGAGTGTGCTTCCAGTGTCCCGCGCGAGTGGAGCCCTCG 181  
DB 976 C-GGCTGGCTGAGCTTGGAGTGTGCTTCCAGTGTCCCGCGCGAGTGGAGCCCTCG 1034  
QY 182 CCCAGTTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTCCCTGCGCGGCC 241  
DB 1035 CCCAGTTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTCCCTGCGCGGCC 1094  
QY 242 AAAGAACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCTCCAGCGACA 301  
DB 1095 AAAGAACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAGCGAGTGCAGAGATCCCGGCAATGAGAGGTTGTCACTATATCTGGTAATG 361

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Db 1155 AGGAACGACGAGTGCAGATCCCGCATGAGAGTGTCTACTATATCTGTTAATG 1214
QY 362 GGAGCATCCACAGCCGGAAGTTTCTCTACATACGTAACCAAGAAATATGGTGTGGTGA 421
Db 1215 GGAGCATCCACAGCCGGAAGTTTCTCTACATACGTAACCAAGAAATATGGTGTGGTGA 1274
QY 422 GATTAGTTGCAGTAGATGAAATGTGCGATCCAGCTGACATTTGATGAGANTTGGC 481
Db 1275 GATTAGTTGCAGTAGATGAAATGTGCGATCCAGCTGACATTTGATGAGANTTGGC 1334
QY 482 TGAAGATCCAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCAGTG 541
Db 1335 TGAAGATCCAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCAGTG 1394
QY 542 ATGGAAGTGTGTTAGAACGCTGGTGTGTTCTGGACTGTGCAGGAAAGCAGACTTCTA 601
Db 1395 ATGGAAGTGTGTTAGAACGCTGGTGTGTTCTGGACTGTGCAGGAAAGCAGACTTCTA 1454
QY 602 AAGGAAATCATATCAGGATPAAGATTGTATCTGATGAGTATTTCCATCTGAACCGGAT 661
Db 1455 AAGGAAATCATATCAGGATPAAGATTGTATCTGATGAGTATTTCCATCTGAACCGGAT 1514
QY 662 TCTGCATCCACTACAGTATTTATGCGCAACAAGTACAGAAACCCAGAGTCTCTCGGTG 721
Db 1515 TCTGCATCCACTACAGTATTTATGCGCAACAAGTACAGAAACCCAGAGTCTCTCGGTG 1574
QY 722 TGCCCCCTTCATCTTTGATGTTGAGACCTGCTCAAAATGCTGTGACTGCTTCAGTACT 781
Db 1575 TGCCCCCTTCATCTTTGATGTTGAGACCTGCTCAAAATGCTGTGACTGCTTCAGTACT 1634
QY 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGCAGTGGACGCTTCT 841
Db 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGGACGCTTCT 1694
QY 842 ACAAGCCAACTGCGAGCTTTTGGCAAGCTTTCTGTATGGGAAAAAAGCAAGTGG 901
Db 1695 ACAAGCCAACTGCGAGCTTTTGGCAAGCTTTCTGTATGGGAAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGNAGAGGTAAACTCTACAGTGTGACACCCCGGAATCTT 961
Db 1755 TGAATCTGAATCTCTCAAGNAGAGGTAAACTCTACAGTGTGACACCCCGGAATCTT 1814
QY 962 CAGTGTCCATACGGAAGAGCTTAAAGAGACAGATACCATATTTCTGGCCAGGTTCTTCC 1021
Db 1815 CAGTGTCCATACGGAAGAGCTTAAAGAGACAGATACCATATTTCTGGCCAGGTTCTTCC 1874
QY 1022 TGGTCAAGCGCTGTGAGAGAAATTTGCTGTGTCTCCATAATTTGCAATGCAATGTCAGT 1081
Db 1875 TGGTCAAGCGCTGTGAGAGAAATTTGCTGTGTCTCCATAATTTGCAATGCAATGTCAGT 1934
QY 1082 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTTCAAGTGTGACCAAAAATG 1141
Db 1935 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTTCAAGTGTGACCAAAAATG 1994
QY 1142 GAGTCAAGGGATGTCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGTG 1201
Db 1995 GAGTCAAGGGATGTCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGTG 2054
QY 1202 ACTGTGTGTAGAGGAAACCCAGAGGGTAACTGACGCTTCTGAGAGCAGCAGTGTGAG 1261
Db 2055 ACTGTGTGTAGAGGAAACCCAGAGGGTAACTGACGCTTCTGAGAGCAGCAGTGTGAG 2114
QY 1262 CACTGGCAATCTGTGTACCCCAAGCAACCTTTCATCCCAAGGAGTGTGGCCGAGGG 1321
Db 2115 CACTGGCAATCTGTGTACCCCAAGCAACCTTTCATCCCAAGGAGTGTGGCCGAGGG 2174
QY 1322 CTCTCAGTGTGTGCTGCTATGTTAAGATCTTACTGTCTCCCAAGCAAAATCTTCAG 1381
Db 2175 CTCTCAGTGTGTGCTGCTATGTTAAGATCTTACTGTCTCCCAAGCAAAATCTTCAG 2234
QY 1382 TTGTTTGTCTCAATAGCCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACCAAGAGGC 1441
Db 2235 TTGTTTGTCTCAATAGCCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACCAAGAGGC 2294
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QY 1442 ACCAANAGGAGTCAATCACAAGCACTGC 1470
Db 2295 ACCAAGAGGAGTCAATCACAAGCACTGC 2323
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US-10-264-361-3
; Sequence 3, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-10-264-361-3
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Query Match 98.0%; Score 1444.8; DB 14; Length 3571;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATCGGATTTATGTGGAACTA 61
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATCGGATTTATGTGGAACTA 915
QY 62 CCTCGGATTTCTCTGTCGACAGCGCGCCAGGCGCTTCCACCGAGCGCAGCCTTTCC 121
Db 916 CCTCGGATTTCTCTGTCGACAGCGCGCCAGGCGCTTCCACCGAGCGCAGCCTTTCC 975
QY 122 CGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAAGCCCTCG 181
Db 976 C-GGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAAGCCCTCG 1034
QY 182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGACATCTGCTGCGCGGC 241
Db 1035 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGACATCTGCTGCGCGGC 1094
QY 242 AAAGAACCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGTCTCTCAGCGACA 301
Db 1095 AAAGAACCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGTCTCTCAGCGACA 1154
QY 302 AGGACACAGAAAGGAGTCAAGATCCCGGATGAGAGAGTGTCTATATCTGTTAATG 361
Db 1155 AGGACACAGAAAGGAGTCAAGATCCCGGATGAGAGAGTGTCTATATCTGTTAATG 1214
QY 362 GGAGCATCCACAGCCGGAAGTTTCTCTATAGTACCAAGAAATATGCTGCTGTGGA 421
Db 1215 GGAGCATCCACAGCCGGAAGTTTCTCTATAGTACCAAGAAATATGCTGCTGTGGA 1274
QY 422 GATTAGTTGCAAGTGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGC 481
Db 1275 GATTAGTTGCAAGTGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGC 1334
QY 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGAGCCAGTG 541
Db 1335 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGAGCCAGTG 1394
QY 542 ATGGAAGTGTGTTAGGAGCGTGTGTTCTGGACTGTGCGGAGTGTGCCAGGAAAGCAGACTTCTA 601
Db 1395 ATGGAAGTGTGTTAGGAGCGTGTGTTCTGGACTGTGCGGAGTGTGCCAGGAAAGCAGACTTCTA 1454
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QY 602 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCATCTGAACCGGAT 661
DB 1455 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCATCTGAACCGGAT 1514
QY 662 TCTGATCCACTACAGTATATCATGCCCAAGATGCACAGAAACCCAGAGTCTTTCGGTGT 721
DB 1515 TCTGATCCACTACAGTATATCATGCCCAAGATGCACAGAAACCCAGAGTCTTTCGGTGT 1574
QY 722 TCGCCCTTCATCTTGTTCATTTGACCTCTCAACAAATCTGTGATGCTGCTTCAGTACCT 781
DB 1575 TCGCCCTTCATCTTGTTCATTTGACCTCTCAACAAATCTGTGATGCTGCTTCAGTACCT 1634
QY 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGCTCT 841
DB 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGCTCT 1694
QY 842 ACAAGCCACATGGCGAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901
DB 1695 ACAAGCCACATGGCAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCT 961
DB 1755 TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCT 1814
QY 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTCC 1021
DB 1815 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTCC 1874
QY 1022 TGGTCAAGGCTGTGGAGAAATGTGCGTGTGCTCCATATTTGCAATGATGTCACT 1081
DB 1875 TGGTCAAGGCTGTGGAGAAATGTGCGTGTGCTCCATATTTGCAATGATGTCACT 1934
QY 1082 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTGACACCAAAAACTG 1141
DB 1935 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTGACACCAAAAACTG 1994
QY 1142 GAGTCAAGGATGCATTAAGTCACTACATGATGTGGCTCTGGAACACCAAGGAAATGTG 1201
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QY 1202 ACTGTGTGTAGAGGAACGAGGAGGTAACTGACGCTTCGTAGCAGCACAGTGG 1261
DB 2055 ACTGTGTGTAGAGGAACGAGGAGGTAACTGACGCTTCGTAGCAGCACAGTGG 2114
QY 1262 CACTGGCATTCGTGTACCCCAAGCAACCTTCATCCCAAGCAAGCTGTGGCCGAGG 1321
DB 2115 CACTGGCATTCGTGTACCCCAAGCAACCTTCATCCCAAGCAAGCTGTGGCCGAGG 2174
QY 1322 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 1381
DB 2175 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 2234
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGACGAGCTTCAAGTGTCTCTTAAAGACCAAGGCG 1441
DB 2235 TTGTTTGTCTCAATAGCTTCCCTGACGAGCTTCCCTGACGAGCTTCAAGTGTCTCTTAAAGACCAAGGCG 2294
QY 1442 ACCAAGAGGATCAATCAAAAGCACTGC 1470
DB 2295 ACCAAGAGGATCAATCAAAAGCACTGC 2323
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## RESULT 6

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US-10-178-442-1
; Sequence 1, Application US/10178442
; Publication No. US20030113870A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: 11669.112USD2
; CURRENT APPLICATION NUMBER: US/10178,442
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 09/265,686
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; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2689)..(2689)
; OTHER INFORMATION: Any nucleotide
US-10-178-442-1
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Query Match 62.0%; Score 914.2; DB 14; Length 2825;
Best Local Similarity 83.5%; Pred. No. 4.6e-296;
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;
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Qy	838	CTCTACAAGCCAAACATGGCAGCTTTTGGGCAAGGCTTTCCCTGTATGGAAAAAAGCAAA	897
Db	901	CTATATAGGCCAACCTTGSCAACTTCTTTGGCAAGGCTTTTGTTTTGAAGAAATCCAGA	960
Qy	898	GTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAACCTCTACAGCTGCACACCCCGGAAC	957
Db	961	GTGGTGGATCTGAACCTTCTAAACAGAGAGGTAGATTATACAGCTGCACACCTCGTAAC	1020
Qy	958	TTCTCAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGT	1017
Db	1021	TTCTCAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCAGGTTGT	1080
Qy	1018	CTCTGTCTCAAGCGCTGTGGAGGAAATGTGCGCTGTTGTCTCCATAATTGCAATGAATGT	1077
Db	1081	CTCTGTGTTAAACGCTGTGGTGGAACTGTGCGCTGTTGTCTCCACAATTGCAATGAATGT	1140
Qy	1078	CAGTGTCTCCACGTAAAGTTACAAAAAGTACCATGAGTGCCTTCAGTTGAGACCAAAA	1137
Db	1141	CAATGTGTCCACAGCAAAGTTACTTAAAAAATACACAGGTGCCTTCAGTTTGAACCAAG	1200
Qy	1138	ACTGGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAAACACCCACGAGAA	1197
Db	1201	ACCGGTGTCAAGGGATTGCACAAATCACTCACCGAGTGGCCCTGGAGCACCATGAGGAG	1260
Qy	1198	TGTGACTGTGTGTAGAGGAAACGACGAGGAGGTAACTGCAGCGCTTCGTAGCAGCAC	1254
Db	1261	TGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGGATCACCAACACGACGCTC	1317

Query Match	62.0%	Score 914.2	DB 11	Length 2839
Best Local Similarity	83.5%	Prod. No. 4.6e-296		
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Db	150	CCCTTGCATTCTCTGCTGCCAGAGCAGGCTCGCGCGCTTCCACCCAGTCAGAGCCTTCCC	209	
QY	122	CGG----GCTGGGGTGAGCCCTTGAGATCGTCTGCTTCCCAAGTCGCCCGCAGTGAGCC	177	
Db	210	TGGCGGTGGTGAAGAGACTCGGAGTCTGCTTCCAAAGTCGCCCGCTGAGTGAGCT	269	
QY	178	CTGCCCCAGTCAGCCAAATGCTCTCTCGGCGCTCTCTCTGTGACATCTGCCCTGGCC	237	
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QY	238	GGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGC	297	
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QY	298	GACAAGGAACAGAACCGAGTGCAGATGCCCGCATGAGAGAGTCTGCACTATCTGTT	357	
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QY	478	GGGCTGGAAGTCCAGAGACGATATATCCAGTAGTATGATTTGTAGAACTTGAGGAGCCC	537	
Db	570	GGGCTTGAAGCCAGAGATGACATATCAAGTAGTATGATTTGTAGAACTTGAGGAGCCC	629	
QY	538	AGTGATGGAAGTCTTTTATAGACGCTGGTGTGTTCTGGGACTGTGTCAGGAAGCAGACT	597	



Db 630 AGTGATGGAATATATTAGGCGCTGTGTGTTCTGCTACTGTACCAAGGAAACAGATT 689  
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QY 658 GGATTCTCATCCACTACAGTATTATCATGCAAGTCAAGAAACCAAGTCTCTTCG 717  
Db 750 GGGTTCTGATCCACTACAAATCTCATGCAACAAATCAAGAGCTGTGATCTTCA 809  
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RESULT 8

US-09-978-295A-487  
; Sequence 487, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630FIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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5 PRIOR APPLICATION NUMBER: 60/084600  
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8 PRIOR FILING DATE: 1998-05-07  
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28 PRIOR FILING DATE: 1998-05-15  
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30 PRIOR FILING DATE: 1998-05-15  
31 PRIOR APPLICATION NUMBER: 60/085697

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Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

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QY 538 ACTGATGGAAGTGTGTTTGGAGCGCTGGTGTGTTCTGGAGCTGTGCCAGAAACAGACT 597

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## RESULT 10

US-09-978-192A-487  
Sequence 487, Application US/09978192A

Patent No. US2002017553A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gramaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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QY	238	GGCCAAAGAACGGGAGCTCGGGCTGAGTCCAACTTGAGCAGCAAGTTGCAGCTCTCC	297
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QY	298	GACAAGGAAACAGAACCGAGTCCAAGATCCCGCGCATGAGAGATTGTCACATATCTG	357
Db	387	AACAGAGAACAGACGAGTACAAGATCCTCAGCATGAGAGATTTATCTGTGCTACT	446
QY	358	AATGGGAGCATCCACAGCCCGAAGTTTCTCATAGTACCCAGAAATATGGTGTGGTG	417
Db	447	AATGGAAGTATTCACAGCCCAAGTTTCTCATACTTATCCAGAAATACGGTCTTGTA	506
QY	418	TGGAGATTAGTTGCAGTAGATGAAAATGTGGCGATCCAGCTGACATTTGATGAGAGAT	477
Db	507	TGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATCAACTTACGTTTGATGAAAGAT	566
QY	478	GGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGAGGCC	537
Db	567	GGGCTTGAACACCCAGAGAGTACATATGCAAGTATGATTTGTAGAAAGTTGAGAAACC	626
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Qy 778 ACCTTGAAGAGCTGATTCGGTACTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGC 837  
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Qy 838 CTCTACAGCCACATGGAGCTTTTGGGCAAGCTTCTCTGTATGGGAAAAAAGCAAA 897  
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Db 1287 TGTGACTGTGTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1343

## RESULT 12

US-09-978-189-487

; Sequence 487, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
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## RESULT 14

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; Sequence 487, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 487  
; LENGTH: 2849  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2715  
; OTHER INFORMATION: unknown base  
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Qy 358 AATGGAGCATTCACAGCCGAGAGTTTCTCTACATGATCCCAAGAAATATGTTGCTGCTG 417  
Db 447 AATGGAGATTTTACAGCCGAGAGTTTCTCTACATGATCCCAAGAAATATGTTGCTGCTG 506  
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER
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; CURRENT FILING DATE: 1999-09-30
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Query Match      99.9%; Score 1473; DB 1; Length 1474;
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Db 1261 GCACTGCGATTTCTGTACCCCAACAGCAACCTTCACTCCCAAGCGTGTGCGCGAGG 1320  
Qy 1321 GCTCTCAGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
Db 1321 GCTCTCAGCTGCTGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
Qy 1381 GTTGTGCTTCAATAGCTTCCCTGCGAGGCTTCAAGTGTCTTTAAAGACCAAGAGG 1440  
Db 1381 GTTGTGCTTCAATAGCTTCCCTGCGAGGCTTCAAGTGTCTTTAAAGACCAAGAGG 1440  
Qy 1441 CACCAANAGAGTCAATCACAAGCACTGCACCG 1474  
Db 1441 CACCAANAGAGTCAATCACAAGCACTGCACCG 1474

## RESULT 2

PCT-US99-22668-6  
; Sequence 6, Application PC/TUS9922668B  
; GENERAL INFORMATION:  
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER  
; CURRENT APPLICATION NUMBER: PCT/US99/22668B  
; CURRENT FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/102,461  
; EARLIER FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/108,109  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 60/110,749  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 60/113,002  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 60/135,426  
; EARLIER FILING DATE: 1999-05-21  
; EARLIER APPLICATION NUMBER: 60/144,022  
; EARLIER FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: a, c, g or t

PCT-US99-22668-6  
Query Match  
Best Local Similarity 99.9%; Score 1473; DB 2; Length 1474;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60  
Db 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60  
Qy 61 ACCCTGGCATTTCTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGCAGCTTTTC 120  
Db 61 ACCCTGGCATTTCTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGCAGCTTTTC 120  
Qy 121 CCGGCTGGGCTGAGCGCTTGGAGTGTGCTTCCAGTGCCTCCAGTGCCTCCAGTGCCTCC 180  
Db 121 CCGGCTGGGCTGAGCGCTTGGAGTGTGCTTCCAGTGCCTCCAGTGCCTCCAGTGCCTCC 180  
Qy 181 GCCCAGTCCAGCAATGCTCTCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Db 181 GCCCAGTCCAGCAATGCT 240  
Qy 241 CAAAGAACGGGACTCGGGCTGAGTCAACTGAGCAGCAAGTTGCACTATCTGTAAT 300  
Db 241 CAAAGAACGGGACTCGGGCTGAGTCAACTGAGCAGCAAGTTGCACTATCTGTAAT 300  
Qy 301 AAGGAACAGAGCGAGTGCAGATCCCGGCTGAGAGTGTGCTATCTGTAAT 360  
Db 301 AAGGAACAGAGCGAGTGCAGATCCCGGCTGAGAGTGTGCTATCTGTAAT 360  
Qy 361 GGGAGCATCCACAGCCCGAAGTTTCTCTATCATGCTACCAAGAAATATGCTGCTGCTG 420  
Db 361 GGGAGCATCCACAGCCCGAAGTTTCTCTATCATGCTACCAAGAAATATGCTGCTGCTG 420  
Qy 421 AGATTAGTGTGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 AGATTAGTGTGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Qy 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGT 540  
Qy 541 GATGGAAGTGTGTTAGGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 541 GATGGAAGTGTGTTAGGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Qy 601 AAAGGAATCATATCAGGATTAAGATTTGCTATCTGATGAGTATTTTCCATCTGAAACCGGA 660  
Db 601 AAAGGAATCATATCAGGATTAAGATTTGCTATCTGATGAGTATTTTCCATCTGAAACCGGA 660  
Qy 661 TTCTGCATCCATCAGTATTTATCATGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 661 TTCTGCATCCATCAGTATTTATCATGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Qy 721 TTGCCCCCTTCTATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 TTGCCCCCTTCTATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 781 TTGGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 781 TTGGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Qy 841 TACAGCCCAACATGCGAGCTTTTGGCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 TACAGCCCAACATGCGAGCTTTTGGCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAATCTTACAGCTGCACACCCCGAACTTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAATCTTACAGCTGCACACCCCGAACTTC 960  
Qy 961 TCAGTGTCCATACGGGAAGAGCTTAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTC 1020  
Db 961 TCAGTGTCCATACGGGAAGAGCTTAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTC 1020

QY 1021 CTGCTCAAGCGCTGTGGAGAAATGTGCTGTGTCTCATTAATTCGAATGATCTCAG 1080  
Db 1021 CTGCTCAAGCGCTGTGGAGAAATGTGCTGTGTCTCATTAATTCGAATGATCTCAG 1080  
QY 1081 TGTGTCCACGTAAGATTACAAAAGAGTACCATGAGTCTCTTCAGTTGAGACCAAAACT 1140  
Db 1081 TGTGTCCACGTAAGATTACAAAAGAGTACCATGAGTCTCTTCAGTTGAGACCAAAACT 1140  
QY 1141 GGAGTCAAGGATTCGTAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGT 1200  
Db 1141 GGAGTCAAGGATTCGTAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGT 1200  
QY 1201 GACTGTGTGTGAGAGAAACGAGAGGTAATCTGAGGCTTCCTAGAGCACACGTGA 1260  
Db 1201 GACTGTGTGTGAGAGAAACGAGAGGTAATCTGAGGCTTCCTAGAGCACACGTGA 1260  
QY 1261 GCACTGGCATCTGTGTGTACCCCAAGCAACCTTCATCCCAAGCAAGCTTCATCCCAAGCAAG 1320  
Db 1261 GCACTGGCATCTGTGTGTACCCCAAGCAACCTTCATCCCAAGCAAGCTTCATCCCAAGCAAG 1320  
QY 1321 GCTCTCAGCTGTGATGTGCTATGTTAAAGTCTTACTGCTTCCAAACCAAAATCTCA 1380  
Db 1321 GCTCTCAGCTGTGATGTGCTATGTTAAAGTCTTACTGCTTCCAAACCAAAATCTCA 1380  
QY 1381 GTTGTGTCTTCAATAGCTTCCCTTCCAGCACTTCAAGTGTCTTCTTAAAGACCAAGAG 1440  
Db 1381 GTTGTGTCTTCAATAGCTTCCCTTCCAGCACTTCAAGTGTCTTCTTAAAGACCAAGAG 1440  
QY 1441 CACCAANAGAGTCAATCAACAAAGCACTGCACCG 1474  
Db 1441 CACCAANAGAGTCAATCAACAAAGCACTGCACCG 1474

## RESULT 3

US-09-410-349A-6  
; Sequence 6, Application US/09410349A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annika  
; APPLICANT: IUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/410,349A  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t  
US-09-410-349A-6

Query Match 99.9%; Score 1473; DB 21; Length 1474;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACCTGGAGACACAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60  
Db 1 CACCTGGAGACACAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60  
QY 61 ACCCTGCGAATCTCTGCTGCCAGAGCGCGCTTCCACCCAGCGAGCCTTTTC 120  
Db 61 ACCCTGCGAATCTCTGCTGCCAGAGCGCGCTTCCACCCAGCGAGCCTTTTC 120  
QY 121 CGGGCTGGGTGAGCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTC 180  
Db 121 CGGGCTGGGTGAGCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTC 180  
QY 181 GCCCAGTCAGCAAAATCTCTCTCGGCTCTCTCTGCTGATCTGCTGCGCCGCG 240  
Db 181 GCCCAGTCAGCAAAATCTCTCTCGGCTCTCTCTGCTGATCTGCTGCGCCGCG 240  
QY 241 CAAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGAGCAAGTTGAGCTCTCCAGGAC 300  
Db 241 CAAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGAGCAAGTTGAGCTCTCCAGGAC 300  
QY 301 AAGGAACAGAGCGAGTCCAAAGATCCCGGCTGAGAGAGTTGCTATATCTGTAAT 360  
Db 301 AAGGAACAGAGCGAGTCCAAAGATCCCGGCTGAGAGAGTTGCTATATCTGTAAT 360  
QY 361 GGGAGCATCCACAGCGCGAAGTTTCTCATACGTAACCAAGAAATATGGTCTGGTGG 420  
Db 361 GGGAGCATCCACAGCGCGAAGTTTCTCATACGTAACCAAGAAATATGGTCTGGTGG 420  
QY 421 AGATTAGTTCAGTAGAGTAAATGTGCGGATCCAGCTGACATTTGAGAGATTTGG 480  
Db 421 AGATTAGTTCAGTAGAGTAAATGTGCGGATCCAGCTGACATTTGAGAGATTTGG 480  
QY 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCAGT 540  
QY 541 GATGGAAGTGTGTTAGGACGCTGTGGTGTCTGGACTGTGCCAGGAAAGCAGACTTCT 600  
Db 541 GATGGAAGTGTGTTAGGACGCTGTGGTGTCTGGACTGTGCCAGGAAAGCAGACTTCT 600  
QY 601 AAAGGAATCATATCAGGATTAAGTATCTGATGAGTATTTTCCATCTGAAACCCGGA 660  
Db 601 AAAGGAATCATATCAGGATTAAGTATCTGATGAGTATTTTCCATCTGAAACCCGGA 660  
QY 661 TTCTGATCCACTACAGTATTTATGATGCAAGTCCAGAAACCAAGAGTCTTCGGTG 720  
Db 661 TTCTGATCCACTACAGTATTTATGATGCAAGTCCAGAAACCAAGAGTCTTCGGTG 720  
QY 721 TTGCCCCCTTCATCTTTGTCAATTCGACTGTCAACATGCTGTGACTTCAGTACC 780  
Db 721 TTGCCCCCTTCATCTTTGTCAATTCGACTGTCAACATGCTGTGACTTCAGTACC 780  
QY 781 TTGGAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGAGCTTGACAGCTC 840  
Db 781 TTGGAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGAGCTTGACAGCTC 840  
QY 841 TACAAGCCCAATGCGAGCTTTTGGGCAAGCTTCTGATGAGAAAGCAAGATG 900  
Db 841 TACAAGCCCAATGCGAGCTTTTGGGCAAGCTTCTGATGAGAAAGCAAGATG 900  
QY 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAATTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAATTC 960  
QY 961 TCAGTGTCCATACCGGAAGAGCTTAAAGAGGACAGATACCATTTCTGGCAGGTTGCTC 1020  
Db 961 TCAGTGTCCATACCGGAAGAGCTTAAAGAGGACAGATACCATTTCTGGCAGGTTGCTC 1020



Db 1021 CTGGTCAAGCGCTGTGGAGAAATTTGGCTGTGTCTCATTAATTCGAATGAATCTCAG 1080  
QY 1081 TGTGTCCCACTAAAGTTTCAAAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACT 1140  
Db 1081 TGTGTCCCACTAAAGTTTCAAAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACT 1140  
QY 1141 GGAGTCAAGGGATTTGATAGTCACTCACTGATGTGGCTGTGGAACACACAGGGAATGT 1200  
Db 1141 GGAGTCAAGGGATTTGATAGTCACTCACTGATGTGGCTGTGGAACACACAGGGAATGT 1200  
QY 1201 GACTGTGTGTGTAGAGAAACGAGGAGGTAACTGACGCTTCGTAGCAGCACAGTGA 1260  
Db 1201 GACTGTGTGTGTAGAGAAACGAGGAGGTAACTGACGCTTCGTAGCAGCACAGTGA 1260  
QY 1261 GCACTGGCAATCTGTGTACCCCAACAACTTCATCCCAACAGCGCTTGGCCGCGAGG 1320  
Db 1261 GCACTGGCAATCTGTGTACCCCAACAACTTCATCCCAACAGCGCTTGGCCGCGAGG 1320  
QY 1321 GCTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTGTCTCCAAACCAATTTCTCA 1380  
Db 1321 GCTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTGTCTCCAAACCAATTTCTCA 1380  
QY 1381 GTTGTGTGCTTCAATAGCTTCCCTCTGCAGGACTTCAAGTGTCTTCTAAAGACACAGG 1440  
Db 1381 GTTGTGTGCTTCAATAGCTTCCCTCTGCAGGACTTCAAGTGTCTTCTAAAGACACAGG 1440  
QY 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474  
Db 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474

RESULT 5

US-09-852-209A-6  
; Sequence 6, Application US/09852209A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t  
US-09-852-209A-6

Query Match 99.9%; Score 1473; DB 35; Length 1474;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACCTGGACACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAAACT 60  
Db 1 CACCTGGACACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAAACT 60  
QY 61 ACCCTGCGATTCTCTGCTCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGCAGCCTTTCC 120  
Db 61 ACCCTGCGATTCTCTGCTCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGCAGCCTTTCC 120  
QY 121 CCGGGCTGGGCTGAGCGTTGGAGTGTCTCTTCCAGTTCGCCCGCGCGAGTGAGCCCTC 180  
Db 121 CCGGGCTGGGCTGAGCGTTGGAGTGTCTCTTCCAGTTCGCCCGCGCGAGTGAGCCCTC 180  
QY 181 GCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGTCACATCTGCCCTGGCGGC 240  
Db 181 GCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGTCACATCTGCCCTGGCGGC 240  
QY 241 CAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCACGAC 300  
Db 241 CAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCACGAC 300  
QY 301 AAGGAACAGAACGGAGTGCAGATCCCGCGCANGAGAGAGTTGTCACTATATCTGTAAAT 360  
Db 301 AAGGAACAGAACGGAGTGCAGATCCCGCGCANGAGAGAGTTGTCACTATATCTGTAAAT 360  
QY 361 GGGAGCATCCACAGCCCCGAAAGTTTCTCATAGTACCCAGAAATATGGTGTGGTGG 420  
Db 361 GGGAGCATCCACAGCCCCGAAAGTTTCTCATAGTACCCAGAAATATGGTGTGGTGG 420  
QY 421 AGATTAGTTGCACTAGATGAAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGG 480  
Db 421 AGATTAGTTGCACTAGATGAAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGG 480  
QY 481 CTGGAAGATCCAGAAAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAAAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGGAGCCAGT 540  
QY 541 GATGGAAGTGTTTAGGAGCGTGGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCT 600  
Db 541 GATGGAAGTGTTTAGGAGCGTGGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCT 600  
QY 601 AAAGAAATCATATCAGGATGAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCCGA 660  
Db 601 AAAGAAATCATATCAGGATGAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCCGA 660  
QY 661 TTCTGCATCCACTACAGTATTTATCATGCGCAAGTCAAGAAACCAAGTCCCTCGGTG 720  
Db 661 TTCTGCATCCACTACAGTATTTATCATGCGCAAGTCAAGAAACCAAGTCCCTCGGTG 720  
QY 721 TTGCCCCCTTCATCTTTGTCTATTTGGACCTGCTCAACATGCTGACCTGCCTTCAGTACC 780  
Db 721 TTGCCCCCTTCATCTTTGTCTATTTGGACCTGCTCAACATGCTGACCTGCCTTCAGTACC 780  
QY 781 TTGGAAGAGCTGATTCGGTACTTAGAGCCAGATCGATGGCAGGTGACTTGGACAGCTC 840  
Db 781 TTGGAAGAGCTGATTCGGTACTTAGAGCCAGATCGATGGCAGGTGACTTGGACAGCTC 840  
QY 841 TACAGCCCAACATGCGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAGCAAGATG 900  
Db 841 TACAGCCCAACATGCGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAGCAAGATG 900  
QY 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGGACTTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGGACTTC 960  
QY 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGCCAGGTGTCTC 1020  
Db 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGCCAGGTGTCTC 1020  
QY 1021 CTGGTCAAGCGCTGTGGAGAAATTTGCTGTGTCTCCATATTTGCAATGATGTGAG 1080



Db 1021 CTGGTCAAGCGCTGTGGAGGAAATTGTGCTGTGTCTCCATAATTGCAATGAATGTCTCAG 1080  
Qy 1081 TGTGTCCACGTAAAGTTACAAAAAGTACCATGAGGTCCCTTCAGTTCAGACCAAAAACT 1140  
Db 1081 TGTGTCCACGTAAAGTTACAAAAAGTACCATGAGGTCCCTTCAGTTCAGACCAAAAACT 1140  
Qy 1141 GGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGAGGAATGT 1200  
Db 1141 GGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGAGGAATGT 1200  
Qy 1201 GACTGTGTGTGTAGAGGAAACGACGAGGGTAACCTGACGCTTCGTAGCAGACACGTGA 1260  
Db 1201 GACTGTGTGTGTAGAGGAAACGACGAGGGTAACCTGACGCTTCGTAGCAGACACGTGA 1260  
Qy 1261 GCACGTGGCATCTGTGTATCCCCCAACCAAGCAACCTTCATCCCCACACGAGGTGGCCGACAG 1320  
Db 1261 GCACGTGGCATCTGTGTATCCCCCAACCAAGCAACCTTCATCCCCACACGAGGTGGCCGACAG 1320  
Qy 1321 GCTCTCAGCTGTGTATGCTGTATGCTATGTAAGATCTTACTGTCTCCAAACCAAAATCTCA 1380  
Db 1321 GCTCTCAGCTGTGTATGCTGTATGCTATGTAAGATCTTACTGTCTCCAAACCAAAATCTCA 1380  
Qy 1381 GTTGTTCCTCAATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACCCAGAGG 1440  
Db 1381 GTTGTTCCTCAATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACCCAGAGG 1440  
Qy 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474  
Db 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474

## RESULT 6

US-10-131-600-6  
; Sequence 6, Application US/10131600  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10/131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t  
US-10-131-600-6

Query Match  
Best Local Similarity 99.9%; Score 1473; DB 46; Length 1474;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CACCTGGAGACACAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACT 60  
Db 1 CACCTGGAGACACAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACT 60  
Qy 61 ACCCTGCCATCTCTGCTGCCAGAGCGCGGCGCTTCCACCGCAGCGAGCCTTCC 120  
Db 61 ACCCTGCCATCTCTGCTGCCAGAGCGCGGCGCTTCCACCGCAGCGAGCCTTCC 120  
Qy 121 CCGGCTCGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTC 180  
Db 121 CCGGCTCGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTC 180  
Qy 181 GCCCAGTTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGC 240  
Db 181 GCCCAGTTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGC 240  
Qy 241 CAAGAAACGAGGAGTCCGAGTCCAACTGAGCAGCAAGTTCGAGCTCTCCAGCGAC 300  
Db 241 CAAGAAACGAGGAGTCCGAGTCCAACTGAGCAGCAAGTTCGAGCTCTCCAGCGAC 300  
Qy 301 AAGGAAACGAGGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCC 360  
Db 301 AAGGAAACGAGGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCC 360  
Qy 361 GGGAGCATCCACAGCCCGAAGTTCCTCATAGTACCAAGAAATATGCTGTGTGG 420  
Db 361 GGGAGCATCCACAGCCCGAAGTTCCTCATAGTACCAAGAAATATGCTGTGTGG 420  
Qy 421 AGATTAGTTCAGTAGTAAATGTCGGATCCAGCTCCAGTTCGACATTTGATGAGAGATTGG 480  
Db 421 AGATTAGTTCAGTAGTAAATGTCGGATCCAGCTCCAGTTCGACATTTGATGAGAGATTGG 480  
Qy 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTCGAGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTCGAGAGCCAGT 540  
Qy 541 GATGGAAGTTCGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
Db 541 GATGGAAGTTCGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
Qy 601 AAAGAAATCATATCAGGATTAAGATTTCTATCTGATGAGTATTTTCCATCTGAACCCGA 660  
Db 601 AAAGAAATCATATCAGGATTAAGATTTCTATCTGATGAGTATTTTCCATCTGAACCCGA 660  
Qy 661 TTCTGCATCCACTACAGTATTTATCATGCCAAGTTCAGAGAAACCAAGTCTTTCGGTG 720  
Db 661 TTCTGCATCCACTACAGTATTTATCATGCCAAGTTCAGAGAAACCAAGTCTTTCGGTG 720  
Qy 721 TTGCCCCCTTCATCTTTGTCACTTGTGAACTGTCTCAACATGCTGACTGCTTCACTACC 780  
Db 721 TTGCCCCCTTCATCTTTGTCACTTGTGAACTGTCTCAACATGCTGACTGCTTCACTACC 780  
Qy 781 TTGGAAGAGCTGATTCGCTACCTAGAGCCAGATCGATGGCAGGTGAGCTTGGACAGCTC 840  
Db 781 TTGGAAGAGCTGATTCGCTACCTAGAGCCAGATCGATGGCAGGTGAGCTTGGACAGCTC 840  
Qy 841 TACAAGCCACATGGCAGCTTTTGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTG 900  
Db 841 TACAAGCCACATGGCAGCTTTTGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTG 900  
Qy 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGAATTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGAATTC 960  
Qy 961 TCAGTGTCCATACGGGAGAGCTTAAAGAGGACAGATACCATTTCTGGCCAGGTGTCTC 1020  
Db 961 TCAGTGTCCATACGGGAGAGCTTAAAGAGGACAGATACCATTTCTGGCCAGGTGTCTC 1020  
Qy 1021 CTGGTCAAGCGCTGTGGAGGAAATTTGTCCTGTGTGTCTCCATAATTGCAATGAATGTCTCAG 1080



```
Db 1021 CTGGTCAAGCGCTGTGGAGGAATTTGTCCTGTTGCTCTCCATAATTTGCAATGAATGTCTAG 1080
Qy 1081 TGTGTCCCAAGTAAAGTTACAAAAGTACCAATGAGTGTCTTCAAGTTGAGACCAAAAACCT 1140
Db 1081 TGTGTCCCAAGTAAAGTTACAAAAGTACCAATGAGTGTCTTCAAGTTGAGACCAAAAACCT 1140
Qy 1141 GGAGTCAAGGATTCGATAAGTCACTCACTGATGTGGCTCTGGAACACCAACAGGAATGT 1200
Db 1141 GGAGTCAAGGATTCGATAAGTCACTCACTGATGTGGCTCTGGAACACCAACAGGAATGT 1200
Qy 1201 GACTGTGTGTGAGAGGAAACGACAGAGGTTAACTGACAGCTTCGTAGCAGCACACGTGA 1260
Db 1201 GACTGTGTGTGAGAGGAAACGACAGAGGTTAACTGACAGCTTCGTAGCAGCACACGTGA 1260
Qy 1261 GCACGTGGATTCGTGTGTACCCCAACAGCAACCTTCATCCCAACAGAGGTTGGCCGACG 1320
Db 1261 GCACGTGGATTCGTGTGTACCCCAACAGCAACCTTCATCCCAACAGAGGTTGGCCGACG 1320
Qy 1321 GCTCTCAGCTGTGATGTGGCTATGTTAAAGATCTTACTCTCTCCAAACCAAAATTTCTCA 1380
Db 1321 GCTCTCAGCTGTGATGTGGCTATGTTAAAGATCTTACTCTCTCCAAACCAAAATTTCTCA 1380
Qy 1381 GTTGTGTGTTCAATAGCTTCCCTGACAGGACTTCAAGTGTCTTCTAAAGACCAAGAGG 1440
Db 1381 GTTGTGTGTTCAATAGCTTCCCTGACAGGACTTCAAGTGTCTTCTAAAGACCAAGAGG 1440
Qy 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474
Db 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474
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## RESULT 7

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US-10-303-997B-6
; Sequence 6, Application US/10303997B
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; APPLICANT: COLLUM, Desaire
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (147)..(147)
; OTHER INFORMATION: can be any of a, c, g, or t
US-10-303-997B-6
```

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Query Match          99.9%; Score 1473; DB 50; Length 1474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CACCTGGAGACACAGAAGGGCTCTAGGAAAAATTTTGGATGGGATTTATCTGGAACCT 60
Db 1 CACCTGGAGACACAGAAGGGCTCTAGGAAAAATTTTGGATGGGATTTATCTGGAACCT 60
Qy 61 ACCCTGGCATTCCTGCTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGCAGCCTTTCC 120
Db 61 ACCCTGGCATTCCTGCTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGCAGCCTTTCC 120
Qy 121 CCGGCTGGCTGAGCCCTTGAGAGTCGTGCTTCCAGTGCCTCCAGTGCCTCCGCGAGTGAGCCCTC 180
Db 121 CCGGCTGGCTGAGCCCTTGAGAGTCGTGCTTCCAGTGCCTCCAGTGCCTCCGCGAGTGAGCCCTC 180
Qy 181 GCCCAGTCAGCAAAATGCTCCTCGGCTCCCTCTGCTGACATCTGCTGACATCTGCTGCGCCG 240
Db 181 GCCCAGTCAGCAAAATGCTCCTCGGCTCCCTCTGCTGACATCTGCTGACATCTGCTGCGCCG 240
Qy 241 CAAAGAACGGGACCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGAC 300
Db 241 CAAAGAACGGGACCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGAC 300
Qy 301 AAGGAAACGAGAGTGCAGATCCCGGCGATGAGAGTTGTCACTATATCTGCTAAT 360
Db 301 AAGGAAACGAGAGTGCAGATCCCGGCGATGAGAGTTGTCACTATATCTGCTAAT 360
Qy 361 GGGACATCCACAGCCCGAAGTTTCTCATAGTACCCAAAGAAATATGCTGCTGCTGCTG 420
Db 361 GGGACATCCACAGCCCGAAGTTTCTCATAGTACCCAAAGAAATATGCTGCTGCTGCTG 420
Qy 421 AGATTAGTTGAGTAGATGAAAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGG 480
Db 421 AGATTAGTTGAGTAGATGAAAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGG 480
Qy 481 CTGGAAGATCCAGAGACGATATATGAAAGTATGATTTTGTAGAAAGTTGAGAGCCCACT 540
Db 481 CTGGAAGATCCAGAGACGATATATGAAAGTATGATTTTGTAGAAAGTTGAGAGCCCACT 540
Qy 541 GATGGAAGTGTTTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 GATGGAAGTGTTTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 AAAGAAATCATATCAGGATAGATTTGTATCTGATGATTTTCCATCTGAAACCCGA 660
Db 601 AAAGAAATCATATCAGGATAGATTTGTATCTGATGATTTTCCATCTGAAACCCGA 660
Qy 661 TTCTGATCCACTACAGTATTTATGATGATTTATGATGATTTATGATGATTTATGATGAT 720
Db 661 TTCTGATCCACTACAGTATTTATGATGATTTATGATGATTTATGATGATTTATGATGAT 720
Qy 721 TTGCCCCCTTCTATCTTTGCTGATTTGATGATTTGATGATTTGATGATTTGATGATTT 780
Db 721 TTGCCCCCTTCTATCTTTGCTGATTTGATGATTTGATGATTTGATGATTTGATGATTT 780
Qy 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGGAGTGGAGTGGAGTGG 840
Db 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGGAGTGGAGTGGAGTGG 840
Qy 841 TACAGCCCAATGCGAGCTTTTGGGCAAGCTTTCCTGATGGAAGAAAAAGCAAGAGT 900
Db 841 TACAGCCCAATGCGAGCTTTTGGGCAAGCTTTCCTGATGGAAGAAAAAGCAAGAGT 900
Qy 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACCTCTACAGTGCACACCCCGGACCTTC 960
Db 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACCTCTACAGTGCACACCCCGGACCTTC 960
Qy 961 TCAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTC 1020
Db 961 TCAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTC 1020
Qy 1021 CTGCTCAAGCGCTGTGAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 CTGCTCAAGCGCTGTGAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
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QY 1081 TGTGTCCCACTAAAGTTACAAAAGTACATGAGTCTCTTCAAGTTGACACCAAAACT 1140  
 DB 1081 TGTGTCCCACTAAAGTTACAAAAGTACATGAGTCTCTTCAAGTTGACACCAAAACT 1140  
 QY 1141 GGAAGTCAAGGATTTGCAATAGTCACTCACTGATGAGTCTCTGGAACACCAAGGAATGT 1200  
 DB 1141 GGAAGTCAAGGATTTGCAATAGTCACTCACTGATGAGTCTCTGGAACACCAAGGAATGT 1200  
 QY 1201 GACTGTGTGTAGAGGAAGGAGGAGGAGTAACTGCAAGCTCTCTGAGCAGCACAGTGA 1260  
 DB 1201 GACTGTGTGTAGAGGAAGGAGGAGGAGTAACTGCAAGCTCTCTGAGCAGCACAGTGA 1260  
 QY 1261 GCACTGGATTTCTGTGTACCCCAAGCAAGCAAGTCTCTGAGGAGTCTCTGAGGAGGAGG 1320  
 DB 1261 GCACTGGATTTCTGTGTACCCCAAGCAAGCAAGTCTCTGAGGAGTCTCTGAGGAGGAGG 1320  
 QY 1321 GCTCTCAGCTGCTGATGCTGGCTATGTTAAAGATCTTACTGCTCTCCAAACCAATTTCTCA 1380  
 DB 1321 GCTCTCAGCTGCTGATGCTGGCTATGTTAAAGATCTTACTGCTCTCCAAACCAATTTCTCA 1380  
 QY 1381 GTTGTGTCTCAATAGCTTTCCCTGAGGAGTCTCAAGTGTCTTCTAAAGACCAAGG 1440  
 DB 1381 GTTGTGTCTCAATAGCTTTCCCTGAGGAGTCTCAAGTGTCTTCTAAAGACCAAGG 1440  
 QY 1441 CACCAAGAGGATCAATCAAGAGGAGTCTGACCG 1474  
 DB 1441 CACCAAGAGGATCAATCAAGAGGAGTCTGACCG 1474

RESULT 8  
 US-09-540-703-3  
 ; Sequence 3, Application US/09540703  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Gilbertson, Debra G.  
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
 ; FILE REFERENCE: 00-12X  
 ; CURRENT APPLICATION NUMBER: US/09/540,703  
 ; CURRENT FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 3571  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1049)...(2086)  
 US-09-540-703-3

Query Match 98.0%; Score 1444.8; DB 24; Length 3571;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
 DB 856 AACTGGAGACACAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915  
 QY 62 CCCTGCGATTTCTGTGCGAGAGCGCGCGAGCGCTTCCACCGAGCGAGCGCTTTCCC 121  
 DB 916 CCCTGCGATTTCTGTGCGAGAGCGCGCGAGCGCTTCCACCGAGCGAGCGCTTTCCC 975  
 QY 122 CCGGCTGGGCTGAGCCTTTGGAGTCTGCTGCTTCCCAAGTGTCCCGCGAGTGAGCCCTCG 181  
 DB 976 C-GGCTGGGCTGAGCCTTTGGAGTCTGCTGCTTCCCAAGTGTCCCGCGAGTGAGCCCTCG 1034  
 QY 182 CCCAGATCAGCAAAATCTCTCTCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241  
 DB 1035 CCCCAGTCCAGCAAAATCTCTCTCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1094  
 QY 242 AAAGAACGGGAGTCTGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 301

DB 1095 AAGAAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGTCAGCTCTCCAGCGACA 1154  
 QY 302 AGGAACAGAACGGAGTGCAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGTAATG 361  
 DB 1155 AGGAACAGAACGGAGTGCAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGTAATG 1214  
 QY 362 GAGGACATCCACAGCGCCGAAGTTTCTCATAGTACCACCAAGAAATATGCTGCTGTTGGA 421  
 DB 1215 GAGGACATCCACAGCGCCGAAGTTTCTCATAGTACCACCAAGAAATATGCTGCTGTTGGA 1274  
 QY 422 GATTAGTTGAGTGTAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
 DB 1275 GATTAGTTGAGTGTAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334  
 QY 482 TGAAGATCCAGAAAGCATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 541  
 DB 1335 TGAAGATCCAGAAAGCATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 1394  
 QY 542 ATGAAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 601  
 DB 1395 ATGAAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1454  
 QY 602 AAGGAATCATATCAGATTAAGATTTGATCTGATGATGATTTTCCATCTGAAACCCGAT 661  
 DB 1455 AAGGAATCATATCAGATTAAGATTTGATCTGATGATGATTTTCCATCTGAAACCCGAT 1514  
 QY 662 TCTGATTCATACATGATTTATGTCACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 721  
 DB 1515 TCTGATTCATACATGATTTATGTCACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1574  
 QY 722 TGCCCCCTTCATCTTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTCAT 781  
 DB 1575 TGCCCCCTTCATCTTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTCATTTGTCAT 1634  
 QY 782 TGGAGAGTCTGATTCGATACCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCT 841  
 DB 1635 TGGAGAGTCTGATTCGATACCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCCT 1694  
 QY 842 ACAAGCAACATGCGAGCTTTTGGGCAAGGCTTTTGGGCAAGGCTTTTGGGCAAGGCTTTTGGG 901  
 DB 1695 ACAAGCAACATGCGAGCTTTTGGGCAAGGCTTTTGGGCAAGGCTTTTGGGCAAGGCTTTTGGG 1754  
 QY 902 TGAATCTGAATCTCTCAAGAGAGGATTAATACTTACAGCTGACACACCCCGAGCTTCT 961  
 DB 1755 TGAATCTGAATCTCTCAAGAGAGGATTAATACTTACAGCTGACACACCCCGAGCTTCT 1814  
 QY 962 CAGTCTCCATACCGGAAGAGCTTAAGAGAGCAGATACCATATTTCTGCGCAGGTTGTCTCC 1021  
 DB 1815 CAGTCTCCATACCGGAAGAGCTTAAGAGAGCAGATACCATATTTCTGCGCAGGTTGTCTCC 1874  
 QY 1022 TGCTCAAGCCTGTGAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081  
 DB 1875 TGCTCAAGCCTGTGAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1934  
 QY 1082 GTGTCCCACTAAAGTTTACAAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAACTG 1141  
 DB 1935 GTGTCCCACTAAAGTTTACAAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAACTG 1994  
 QY 1142 GAGTCAAGAGGATTTGCAATAGTCACTCATGATGTGGCTCTGGAACACACAGAGAAATGT 1201  
 DB 1995 GAGTCAAGAGGATTTGCAATAGTCACTCATGATGTGGCTCTGGAACACACAGAGAAATGT 2054  
 QY 1202 ACTGTGTGTAGAGAAACCGCAGGAGGATTAAGTCTGAGCTTCTGAGCAGCACACGCTGAG 1261  
 DB 2055 ACTGTGTGTAGAGAAACCGCAGGAGGATTAAGTCTGAGCTTCTGAGCAGCACACGCTGAG 2114  
 QY 1262 CACTGGCATTTCTGTGTACCCCAAGCAACTTCACTCCCAAGCAGGTTGGCGCAGGG 1321  
 DB 2115 CACTGGCATTTCTGTGTACCCCAAGCAACTTCACTCCCAAGCAGGTTGGCGCAGGG 2174  
 QY 1322 CTCTCAGCTCTGATCTGGCTATGTTAAAGATCTTACTGCTCTCCAAACCAAAATTTCTCAG 1381  
 DB 2175 CTCTCAGCTCTGATCTGGCTATGTTAAAGATCTTACTGCTCTCCAAACCAAAATTTCTCAG 2234

QY 1382 TTGTTTGCTCAATAGACCTCCCTGCGAGACTTCAAGTGTCTTCTTAAAGACAGAGGC 1441  
Db 2235 TTGTTTGCTCAATAGACCTCCCTGCGAGACTTCAAGTGTCTTCTTAAAGACAGAGGC 2294  
QY 1442 ACCAANAGGAGTCAATCAAGAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCAAGAGCACTGC 2323

## RESULT 9

US-09-541-752-42  
; Sequence 42, Application US/09541752  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/541,752  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-541-752-42

Query Match 98.0%; Score 1444.8; DB 24; Length 3571;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1460; Conservative 8; Mismatches 1; Gaps 1;

QY 2 ACCTGGAGACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 856 AACTGGAGACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACTA 915  
QY 62 CCTCGCATCTCTGCTGCGAGCGCGCGAGCGCTTCCACCGCAGCGAGCGCTTTCCC 121  
Db 916 CCTCGCATCTCTGCTGCGAGCGCGCGAGCGCTTCCACCGCAGCGAGCGCTTTCCC 975  
QY 122 CGGGCTGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCGCTCG 181  
Db 976 C-GGCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCGCTCG 1034  
QY 182 CCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGACATCTGCGCTGCGCGGC 241  
Db 1035 CCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGACATCTGCGCTGCGCGGC 1094  
QY 242 AAGAACGGGACTCGGCTGAGTCCACCTGAGCAGCAAGTTGACGCTCTCCAGCGACA 301  
Db 1095 AAGAACGGGACTCGGCTGAGTCCACCTGAGCAGCAAGTTGACGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGAGTTGTCACTATATCTGGTAATG 361  
Db 1155 AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGAGTTGTCACTATATCTGGTAATG 1214  
QY 362 GGAGATCCAGACCGCGAAGTTCTCTATACGTACCCAGAAATATGCTGCTGTGTGGA 421  
Db 1215 GGAGATCCAGACCGCGAAGTTCTCTATACGTACCCAGAAATATGCTGCTGTGTGGA 1274  
QY 422 GATTAGTTCAGTATGATGAAATGTGGATCCAGCTGACATCTTGTATGAGAGATTGGGC 481  
Db 1275 GATTAGTTCAGTATGATGAAATGTGGATCCAGCTGACATCTTGTATGAGAGATTGGGC 1334  
QY 482 TGGAAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTTGGAGGCCAGTG 541

## RESULT 10

US-09-695-121-3

; Sequence 3, Application US/09695121

; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.

;; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS

;; FILE REFERENCE: 00-53

;; CURRENT APPLICATION NUMBER: US/09/695,121

;; CURRENT FILING DATE: 2000-10-23

;; NUMBER OF SEQ ID NOS: 18

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 3

;; LENGTH: 3571

;; TYPE: DNA

;; ORGANISM: Mus musculus

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (1049)...(2086)

US-09-695-121-3

Query Match 98.0%; Score 1444.8; DB 30; Length 3571;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1460; Conservative 8; Mismatches 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGGAACCTA 61  
DB AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGGAACCTA 915  
QY 62 CCTCGGATTTCTCTGCTCCAGAGCGGCGCCAGCGCTTCCACCGAGCGAGCCCTTCC 121  
DB CCTCGGATTTCTCTGCTCCAGAGCGGCGCCAGCGCTTCCACCGAGCGAGCCCTTCC 975  
QY 122 CGGGCTGGGCTAGCCTTGGAGTCTGCTCTCCAGTGCCTCCGCGCGAGTGCAGCCCTCG 181  
DB C-GGCTGGGCTAGCCTTGGAGTCTGCTCTCCAGTGCCTCCGCGCGAGTGCAGCCCTCG 1034  
QY 182 CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGGCC 241  
DB CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGGCC 1094  
QY 242 AAAGAACCGGGGACTCGGGCTGAGTCAACCTGAGCAGCAAGTTGACGCTCTCCAGGACA 301  
DB AAAGAACCGGGGACTCGGGCTGAGTCAACCTGAGCAGCAAGTTGACGCTCTCCAGGACA 1154  
QY 302 AGGACACAGAGGAGTGCAGATCCCGGCGATGAGAGGTTGTCATATCTGGTAATG 361  
DB AGGACACAGAGGAGTGCAGATCCCGGCGATGAGAGGTTGTCATATCTGGTAATG 1214  
QY 362 GGAGCATCCACAGCCCGAGTTTCTCTATACGTACCAAGAAATATGCTGCTGGGA 421  
DB GGAGCATCCACAGCCCGAGTTTCTCTATACGTACCAAGAAATATGCTGCTGGGA 1274  
QY 422 GATTAGTTCAGTAAATGTCGGGATCCAGCTGACATTTGATGAGAGTTTGGGC 481  
DB GATTAGTTCAGTAAATGTCGGGATCCAGCTGACATTTGATGAGAGTTTGGGC 1334  
QY 482 TGGAGATCCAGAGCAGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 541  
DB TGGAGATCCAGAGCAGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 1394  
QY 542 ATGGAAGTGTTTTGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 601  
DB ATGGAAGTGTTTTGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1454  
QY 602 AAGGAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT 661  
DB AAGGAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT 1514  
QY 662 TCTGCATCCACTACGATTTATCATGCAAGTTCACAGAAACACAGAGTCTTCTGGTGT 721  
DB TCTGCATCCACTACGATTTATCATGCAAGTTCACAGAAACACAGAGTCTTCTGGTGT 1574  
QY 722 TGCCCTTCTATCTTCTGATGACCTGCTCAACATGCTGACCTGCTGACCTTCACTACCT 781  
DB TGCCCTTCTATCTTGTGATGACCTGCTCAACATGCTGACCTGCTGACCTTCACTACCT 1634  
QY 782 TGAAGAGCTGATTCGGTACTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 841  
DB TGAAGAGCTGATTCGGTACTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCTCT

RESULT 11

US-09-706-968-42  
; Sequence 42, Application US/09706968  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)

DB 1635 TGAAGAGCTGATTGGTACTAGAGCCAGATCGATGCGAGTGGACTTGGACAGCTCT 1694  
QY 842 ACAAGCCAAACATGGCAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901  
DB 1695 ACAAGCCAAACATGGCAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGAGAGGCTAAACACTACAGCTGCACACCCCGAACTTCT 961  
DB 1755 TGAATCTGAATCTCTCAAGAGAGGCTAAACACTACAGCTGCACACCCCGAACTTCT 1814  
QY 962 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCTCC 1021  
DB 1815 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCTCC 1874  
QY 1022 TGGTCAAGCGCTGTGGAGAAATTTGTCTGTCTCCATTAATTTGCAATGATGTCAGT 1081  
DB 1875 TGGTCAAGCGCTGTGGAGAAATTTGTCTGTCTCCATTAATTTGCAATGATGTCAGT 1934  
QY 1082 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTTCCAGTTGAGACCAAAAACTG 1141  
DB 1935 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTTCCAGTTGAGACCAAAAACTG 1994  
QY 1142 GAGTCAAGGATTTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGTG 1201  
DB 1995 GAGTCAAGGATTTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAAAACGAGAGGTAACCTGAGGCTTCTGAGCAGTTCGAGCAGTGCAG 1261  
DB 2055 ACTGTGTGTAGAGGAAAACGAGAGGTAACCTGAGGCTTCTGAGCAGTTCGAGCAGTGCAG 2114  
QY 1262 GACTGGCATTTCTGTATACCCCAAGCAACCTTCATCCCAAGGCTTGGCCGAGG 1321  
DB 2115 GACTGGCATTTCTGTATACCCCAAGCAACCTTCATCCCAAGGCTTGGCCGAGG 2174  
QY 1322 CTTCTAGCTGTGATGCTGGCTATGTTAAAGATCTTACTCGTCTCAACCAAAATTTCTCAG 1381  
DB 2175 CTTCTAGCTGTGATGCTGGCTATGTTAAAGATCTTACTCGTCTCAACCAAAATTTCTCAG 2234  
QY 1382 TTGTTTGTCTTAATAGCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGGAGC 1441  
DB 2235 TTGTTTGTCTTAATAGCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGGAGC 2294  
QY 1442 ACCAAGAGGATCAATCACAAGCACTGC 1470  
DB 2295 ACCAAGAGGATCAATCACAAGCACTGC 2323

US-09-706-968-42									
Query Match 98.0%; Score 1444.8; DB 31; Length 3571;									
Best Local Similarity 99.4%; Pred. No. 0;									
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;									
QY	2	ACCTGGAGACACAGAGAGGCTCTAGGAAATTTTCGATGGGATTTATGTGGAACCTA	61						
DB	856	AACCTGGAGACACAGAGAGGCTCTAGGAAATTTTCGATGGGATTTATGTGGAACCTA	915						
QY	62	CCCTGGATTTCTCTGCTGACAGCGCGCCAGCGCTTCCACCGAGCGAGCTTTCCC	121						
DB	916	CCCTGGATTTCTCTGCTGACAGCGCGCCAGCGCTTCCACCGAGCGAGCTTTCCC	975						
QY	122	CGGCTGGGCTGAGCCCTTGGAGTGTCTGCTTCCAGTGTCCCGCGGAGTGAGCCCTCG	181						
DB	976	C-GGCTGGGCTGAGCCCTTGGAGTGTCTGCTTCCAGTGTCCCGCGGAGTGAGCCCTCG	1034						
QY	182	CCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG	241						
DB	1035	CCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG	1094						
QY	242	AAAGAACGGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGCGACA	301						
DB	1095	AAAGAACGGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGCGACA	1154						
QY	302	AGGAACAGACGGAGTCAAGATCCCGCATCAGAGAGTTGTCATATATCTGTTAATG	361						
DB	1155	AGGAACAGACGGAGTCAAGATCCCGCATCAGAGAGTTGTCATATATCTGTTAATG	1214						
QY	362	GGAGCATCCACAGCCCGAAGTTTCTCTATACGTACCCAAAGAAATATGGTGTGGGA	421						
DB	1215	GGAGCATCCACAGCCCGAAGTTTCTCTATACGTACCCAAAGAAATATGGTGTGGGA	1274						
QY	422	GATTAGTTCAGTAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC	481						
DB	1275	GATTAGTTCAGTAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC	1334						
QY	482	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTGAGAGTTGAGAGCCAGTG	541						
DB	1335	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTGAGAGTTGAGAGCCAGTG	1394						
QY	542	ATGGAAGTGTTTAGGACGCTGCTGTGTGTTCTGGGACTGTGCGAGAAAGCAGACTTCTA	601						
DB	1395	ATGGAAGTGTTTAGGACGCTGCTGTGTGTTCTGGGACTGTGCGAGAAAGCAGACTTCTA	1454						
QY	602	AAGGAATCATATCAGATTAAGATTTGTATCTGATGATTTTCCATCTGAACCGGAT	661						
DB	1455	AAGGAATCATATCAGATTAAGATTTGTATCTGATGATTTTCCATCTGAACCGGAT	1514						
QY	662	TCTGCACTCACTACAGTATTATCATGCCACAAGTCAAGAAACACAGAGTCCCTTCGGTGT	721						
DB	1515	TCTGCACTCACTACAGTATTATCATGCCACAAGTCAAGAAACACAGAGTCCCTTCGGTGT	1574						
QY	722	TGCCCCCTTCATCTTGTCTATTTGACCTGTCTCAACATGCTGTGACTGCTTCAGTACCT	781						
DB	1575	TGCCCCCTTCATCTTGTCTATTTGACCTGTCTCAACATGCTGTGACTGCTTCAGTACCT	1634						
QY	782	TGGAGAGCTGATTTCGGTACTAGACCGAGATCCATGCGAGGTGGACTTGGACGCTCT	841						
DB	1635	TGGAGAGCTGATTTCGGTACTAGACCGAGATCCATGCGAGGTGGACTTGGACGCTCT	1694						
QY	842	ACAGCCAAACATGCGAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAGTGG	901						
DB	1695	ACAGCCAAACATGCGAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAGTGG	1754						
QY	902	TGAATCTGAATCTCTCAAGGAAAGAGGTAAATCTACAGTGTGACACCCCGGAATCTCT	961						
DB	1755	TGAATCTGAATCTCTCAAGGAAAGAGGTAAATCTACAGTGTGACACCCCGGAATCTCT	1814						
QY	962	CAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATCTTGGCCAGGTGTCTCC	1021						
DB	1815	CAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATCTTGGCCAGGTGTCTCC	1874						
RESULT 12									
US-09-823-033-3									
; Sequence 3, Application US/09823033									
; GENERAL INFORMATION:									
; APPLICANT: Hart, Charles E.									
; APPLICANT: Gilbertson, Debra G.									
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,									
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE									
; FILE REFERENCE: 00-12									
; CURRENT APPLICATION NUMBER: US/09/823,033									
; CURRENT FILING DATE: 2001-03-29									
; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 3									
; LENGTH: 3571									
; TYPE: DNA									
; ORGANISM: Mus musculus									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1049)....(2086)									
US-09-823-033-3									
Query Match 98.0%; Score 1444.8; DB 34; Length 3571;									
Best Local Similarity 99.4%; Pred. No. 0;									
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;									
QY	2	ACCTGGAGACACAGAGAGGCTCTAGGAAATTTTCGATGGGATTTATGTGGAACCTA	61						
DB	856	AACCTGGAGACACAGAGAGGCTCTAGGAAATTTTCGATGGGATTTATGTGGAACCTA	915						
QY	62	CCCTGGATTTCTCTGCTGACAGCGCGCCAGCGCTTCCACCGAGCGAGCTTTCCC	121						
DB	916	CCCTGGATTTCTCTGCTGACAGCGCGCCAGCGCTTCCACCGAGCGAGCTTTCCC	975						
QY	122	CGGCTGGGCTGAGCCCTTGGAGTGTCTGCTTCCAGTGTCCCGCGGAGTGAGCCCTCG	181						
DB	976	C-GGCTGGGCTGAGCCCTTGGAGTGTCTGCTTCCAGTGTCCCGCGGAGTGAGCCCTCG	1034						
QY	182	CCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG	241						

Db 1035 CCCCAGTCAGCCAAATGCTCTCTCTCGGCCCTCTCTCTGCTGACATCTGCGCCCTGCGCGGCC 1094  
Qy 242 AAGAACGGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 301  
Db 1095 AAGAACGGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACGGAGTGCAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGTAATG 361  
Db 1155 AGGAACAGAACGGAGTGCAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGTAATG 1214  
Qy 362 GGAGCATCCACAGCCCGAAGTTTCTCTATAGTACCCCAAGAAATATGGTGTGTGGA 421  
Db 1215 GGAGCATCCACAGCCCGAAGTTTCTCTATACATACCCCAAGAAATATGGTGTGTGGA 1274  
Qy 422 GATTAGTTGAGTAGATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
Db 1275 GATTAGTTGAGTAGATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334  
Qy 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTGTTAGAGTTGAGAGCCCAAGTG 541  
Db 1335 TGAAGATCCAGAGACGATATATGCAAGTATGATTTGTTAGAGTTGAGAGCCCAAGTG 1394  
Qy 542 ATGAGAGTTTATGAGACGCTGTTGTTCTGGACTGTGCCAGGAAAGCAGACTTCTA 601  
Db 1395 ATGAGAGTTTATGAGACGCTGTTGTTCTGGACTGTGCCAGGAAAGCAGACTTCTA 1454  
Qy 602 AAGGAATCATATCAGATAGATTTGTATCTGATGAGTATTTCCACTCTGAACCCCGAT 661  
Db 1455 AAGGAATCATATCAGATAGATTTGTATCTGATGAGTATTTCCACTCTGAACCCCGAT 1514  
Qy 662 TCTGCATCCACTCAGTATATATGCGCAAGTCAAGTCAAGAACCAAGTCTTCCGTTGT 721  
Db 1515 TCTGCATCCACTCAGTATATATGCGCAAGTCAAGTCAAGAACCAAGTCTTCCGTTGT 1574  
Qy 722 TGCCCTCTCATCTTTGCTATTGACCTGTCTCAACATGCTGACCTTCAGTACCT 781  
Db 1575 TGCCCTCTCATCTTTGCTATTGACCTGTCTCAACATGCTGACCTTCAGTACCT 1634  
Qy 782 TGAAGAGCTGATTTCGGTACTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 841  
Db 1635 TGAAGAGCTGATTTCGGTACTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 1694  
Qy 842 ACAAGCCAAATGCGAGCTTTTGGCAAGCTTTCCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAAATGCGAGCTTTTGGCAAGCTTTCCTGTATGGGAAAAAAGCAAGTGG 1754  
Qy 902 TGAATCTGAATCTCTCAAGAGAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTT 961  
Db 1755 TGAATCTGAATCTCTCAAGAGAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTT 1814  
Qy 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTGCGCCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTGCGCCAGGTTGTCTCC 1874  
Qy 1022 TGCTCAAGCGCTGTGAGGAAATTTGCGCTGTGTCTCCATAATTCGAATGAATGTCAGT 1081  
Db 1875 TGCTCAAGCGCTGTGAGGAAATTTGCGCTGTGTCTCCATAATTCGAATGAATGTCAGT 1934  
Qy 1082 GTGTCCCACTGTAAGTTTACAAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAACTG 1141  
Db 1935 GTGTCCCACTGTAAGTTTACAAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAACTG 1994  
Qy 1142 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAAACCAAGAGGAATGTG 1201  
Db 1995 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAAACCAAGAGGAATGTG 2054  
Qy 1202 ACTGTGTGTAGAGGAAACGAGGAGGGTAACTGACGCTTCTGACAGCACACGTCAG 1261  
Db 2055 ACTGTGTGTAGAGGAAACGAGGAGGGTAACTGACGCTTCTGACAGCACACGTCAG 2114  
Qy 1262 CACTGGCATCTGTGTATCCCCCAAGCAACCTTTCATCCCAACAGGTTGGCGGAGG 1321

## RESULT 13

US-10-139-583-42  
; Sequence 42, Application US/10139583  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Glibertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10/139,583  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR FILING DATE: 09/457,066  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-10-139-583-42

Query Match 98.0%; Score 1444.8; DB 46; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 ACCTGGAGACACAGAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 856 AACTGGAGACACAGAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACTA 915  
Qy 62 CCCTGGATTTCTCTGTCGCGAGAGCGCGGCTTCCACCGCAGCGAGCCTTTTCCC 121  
Db 916 CCCTGGATTTCTCTGTCGCGAGAGCGCGGCTTCCACCGCAGCGAGCCTTTTCCC 975  
Qy 122 CGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG 1034  
Qy 182 CCCAGTCAACCAATGCTCTCTCTGCGCTCTCTCTGCTGACATCTGCGCTGCGCGCC 241  
Db 1035 CCCAGTCAACCAATGCTCTCTCTGCGCTCTCTCTGCTGACATCTGCGCTGCGCGCC 1094  
Qy 242 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 301  
Db 1095 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACGGAGTGCAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGTAATG 361  
Db 1155 AGGAACAGAACGGAGTGCAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGTAATG 1214  
Qy 362 GGAGCATCCACAGCCCGAAGTTTCTCTATACGTAACCAAGAAATATGGTGTGTGGA 421







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Db 1515 TCTGATCACTACAGTATTATCATGCCACAAGTCACAGAAACCAGAGCTCTCGGTGT 1574
QY 722 TGGCCCTTCATCTTGTGATTTGGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 781
Db 1575 TGGCCCTTCATCTTGTGATTTGGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 1634
QY 782 TGGAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGTGGACTTGGACAGCTCT 841
Db 1635 TGGAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGTGGACTTGGACAGCTCT 1694
QY 842 ACAAGCCAAATCGGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 901
Db 1695 ACAAGCCAAATCGGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGGAGAGTAAACTCTACAGCTGCACACCCCGAACTTCT 961
Db 1755 TGAATCTGAATCTCTCAAGGAGAGTAAACTCTACAGCTGCACACCCCGAACTTCT 1814
QY 962 CAGTGTCCATACGGGAAGACTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTCC 1021
Db 1815 CAGTGTCCATACGGGAAGACTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTCC 1874
QY 1022 TGTCAAGCGCTGTGAGGAAATTTGGCTTGTCTCCATTAATTCGAATGAATGTCACT 1081
Db 1875 TGTCAAGCGCTGTGAGGAAATTTGGCTTGTCTCCATTAATTCGAATGAATGTCACT 1934
QY 1082 GTGTCCCACTAAAGTTTACAAAAGCTTACCATGAGGTCTTCAAGTTTGAGACCAAAACTG 1141
Db 1935 GTGTCCCACTAAAGTTTACAAAAGCTTACCATGAGGTCTTCAAGTTTGAGACCAAAACTG 1994
QY 1142 GAGTCAAGGATTTGCATAAGTCACTCACTGATGGCTCTGGAACACCCAGGAAATGTG 1201
Db 1995 GAGTCAAGGATTTGCATAAGTCACTCACTGATGGCTCTGGAACACCCAGGAAATGTG 2054
QY 1202 ACTGTGTGTAGAGAAAGCGAGGAGGTAACTGACAGCTTCGTAGCAGCACACGTGAG 1261
Db 2055 ACTGTGTGTAGAGAAAGCGAGGAGGTAACTGACAGCTTCGTAGCAGCACACGTGAG 2114
QY 1262 CACTGGCATCTGTGTACCCCAACAGCAACCTTCATCCCAACAGGTTGGCGCAGGG 1321
Db 2115 CACTGGCATCTGTGTACCCCAACAGCAACCTTCATCCCAACAGGTTGGCGCAGGG 2174
QY 1322 CTCTCAGCTGCTGATGTGCTATAGGTAAAGATCTTACTGCTCTCAACCAAAATCTCTAG 1381
Db 2175 CTCTCAGCTGCTGATGTGCTATAGGTAAAGATCTTACTGCTCTCAACCAAAATCTCTAG 2234
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGCGAGGACTTCAAGTGTCTTAAAGACAGAGGC 1441
Db 2235 TTGTTTGTCTCAATAGCTTCCCTGCGAGGACTTCAAGTGTCTTAAAGACAGAGGC 2294
QY 1442 ACCAANAGGAGTCAATCACAAGACACTGC 1470
Db 2295 ACCAAGAGGAGTCAATCACAAGACACTGC 2323
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## RESULT 15

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US-09-104-216-34
; Sequence 34, Application US/09304216
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19X
; CURRENT APPLICATION NUMBER: US/09/304,216
; CURRENT FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049) ... (2086)
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US-09-304-216-34

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Query Match 97.2%; Score 1432.8; DB 19; Length 3573;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 2 AACTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61
Db 856 AACTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915
QY 62 CCCTGCGATTCTCTGCTGCCAGAGCGCGCAGCGCTTCCACCGCAGCGAGCTTTTCCC 121
Db 916 CCCTGCGATTCTCTGCTGCCAGAGCGCGCAGCGCTTCCACCGCAGCGAGCTTTTCCC 975
QY 122 CGGGCTGGGCTGAGCCCTTGGAGTCGTCTCCCGAGTCCCGCGGAGTGGCCCTCG 181
Db 976 C-GGGCTGGGCTGAGCCCTTGGAGTCGTCTCCCGAGTCCCGCGGAGTGGCCCTCG 1034
QY 182 CCCAGCTCAGCCAAATGCTCTCCGCTCTCTCTGCTGACATCTGCCCTCGCCGCGCC 241
Db 1035 CCCAGCTCAGCCAAATGCTCTCTCCGCTCTCTCTGCTGACATCTGCCCTCGCCGCGCC 1094
QY 242 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA 301
Db 1095 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA 1154
QY 302 AGGAACAGACCGGAGTGCAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 361
Db 1155 AGGAACAGACCGGAGTGCAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214
QY 362 GGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAGCAAAATATGGTCTGTGTGGA 421
Db 1215 GGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAGCAAAATATGGTCTGTGTGGA 1274
QY 422 GATTAGTTCAGTATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481
Db 1275 GATTAGTTCAGTATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334
QY 482 TGGAAATCCAGAAAGCATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 541
Db 1335 TGGAAATCCAGAAAGCATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 1394
QY 542 ATGGAAGTGTTTTGGAGCGCTGTGTGTTCTGGACTGTGCCAGAAAGCAGACTTCTA 601
Db 1395 ATGGAAGTGTTTTGGAGCGCTGTGTGTTCTGGACTGTGCCAGAAAGCAGACTTCTA 1454
QY 602 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTTGAACCCGGAT 661
Db 1455 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTTGAACCCGGAT 1514
QY 662 TCTGCATCCATACAGTATATCATGCCCAAGTCCAGAAACCCAGGTCCTTCGGTGT 721
Db 1515 TCTGCATCCATACAGTATATCATGCCCAAGTCCAGAAACCCAGGTCCTTCGGTGT 1574
QY 722 TGCCCTTCATCTTGTGCTCAACTGCTCAACATGCTGTGACTGCCTTCAGTACCT 781
Db 1575 TGCCCTTCATCTTGTGCTCAACTGCTCAACATGCTGTGACTGCCTTCAGTACCT 1634
QY 782 TGGAAAGAGTGTATTCGGTACCTAGAGCCAGATCGATGGCAGGTTGAGTGGACAGCTCT 841
Db 1635 TGGAAAGAGTGTATTCGGTACCTAGAGCCAGATCGATGGCAGGTTGAGTGGACAGCTCT 1694
QY 842 ACAAGCCAAATCGGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 901
Db 1695 ACAAGCCAAATCGGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGGAGAGGTAATACTTACAGCTGCACACCCCGAACTTCT 961
Db 1755 TGAATCTGAATCTCTCAAGGAGAGGTAATACTTACAGCTGCACACCCCGAACTTCT 1814
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QY	962	CAGTGTCCATACGGGAAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC	1021
Db	1815		
QY	1022	TGGTCAAGCGCTGTGAGGAAATGTGCTTGTCTCCATAATTTGCAATGAATGTCACT	1081
Db	1875		
QY	1082	GTGTCCACGTTAAAGTTACAAAAGTACCATGAGTCTTCTAGTTGAGACCAAAAACCTG	1141
Db	1935		
QY	1142	GAGTCAAGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAATGTG	1201
Db	1995		
QY	1202	ACTGTGTGTAGAGGAAACGAGGAGGTAACTGCAGCCTTCTGTAGCAGCACACGTGAG	1261
Db	2055		
QY	1262	CAGTGGCATTCTGTACCCCC--ACAAGCAACCTTCATCCCAACGAGCGTTGGCCGCGAG	1319
Db	2115		
QY	1320	GGCTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTC	1379
Db	2175		
QY	1380	AGTGTGTTGCTTCAATAGCCTTCCCTGCAGGACTTCAAGTGTCTTCTAAAGACCCAGAG	1439
Db	2235		
QY	1440	GCACCAANAGGAGTCAATCAAAAGCACTGC	1470
Db	2295		

Search completed: November 26, 2003, 08:55:02  
Job time : 3152.15 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 00:11:41 ; Search time 272.739 Seconds  
(without alignments)  
9894.257 Million cell updates/sec

Title: US-09-852-209A-6  
Perfect score: 1474  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2523179 seqs, 915383134 residues

Total number of hits satisfying chosen parameters: 5046358

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq.\*  
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7: /cgn2\_6/prodata/1/pna/US12\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1444.8	98.0	3571	5	US-09-457-066-42
2	1444.8	98.0	3571	5	US-09-876-813-34
3	1444.8	98.0	3571	6	US-10-664-432-3
4	914.2	62.0	3007	1	PCT-US03-26491-58
5	914.2	62.0	3007	6	US-10-648-593-58
6	914.2	62.0	3007	7	US-60-507-511-2084
7	913.8	62.0	3007	7	US-60-487-610-231
8	913.8	62.0	3007	7	US-60-485-450-137
9	912.6	61.9	2779	5	US-09-830-320A-8
10	878.8	59.6	1760	5	US-09-457-066-1
11	878.8	59.6	1760	5	US-09-876-813-32
12	878.8	59.6	1760	6	US-10-664-432-1
13	745.8	50.6	1095	5	US-09-457-066-50
14	660.8	40.6	1035	5	US-09-457-066-6
15	519	35.2	918	1	PCT-US00-28803-6
16	221.8	15.0	221510	7	US-60-487-610-19346
17	221.8	15.0	221510	7	US-60-485-450-11913
18	175	11.9	1110	7	US-09-876-813-6
19	137.2	9.3	1113	6	US-10-321-962-7
20	137.2	9.3	1472	5	US-09-876-813-52
21	137.2	9.3	1472	6	US-10-606-055-3
22	124	8.4	1829	6	US-10-321-962-3
23	123.2	8.4	1882	5	US-09-457-066-36
24	123.2	8.4	1882	5	US-09-876-813-1
25	123.2	8.4	1882	6	US-10-606-055-1
26	119.2	8.1	1587	6	US-10-321-962-5

27	105.6	7.2	135	5	US-09-540-233D-96491	Sequence 96491, A
28	102.6	7.0	462	6	US-10-321-962-11	Sequence 11, Appl
29	84.4	5.7	201	7	US-60-487-610-5053	Sequence 5053, Ap
30	84.4	5.7	201	7	US-60-487-610-32074	Sequence 32074, A
31	84.4	5.7	201	7	US-60-485-450-3279	Sequence 3279, Ap
32	84.4	5.7	201	7	US-60-485-450-19018	Sequence 19018, A
33	82.2	5.6	898	6	US-10-321-962-9	Sequence 9, Appl
34	60.8	4.1	173	1	PCT-US03-26220-26739	Sequence 26739, A
35	40.4	2.7	1176	7	US-60-485-450-651	Sequence 651, App
36	40.4	2.7	14575	7	US-60-485-450-12172	Sequence 12172, A
37	39.6	2.7	201	7	US-60-487-610-5054	Sequence 5054, Ap
38	39.6	2.7	201	7	US-60-487-610-32070	Sequence 32070, A
39	39.6	2.7	201	7	US-60-485-450-3280	Sequence 3280, A
40	39.6	2.7	201	7	US-60-485-450-19014	Sequence 19014, A
41	39.6	2.7	415	6	US-10-321-962-13	Sequence 13, Appl
42	39.4	2.7	17493	7	US-60-485-450-12170	Sequence 12170, A
43	37.6	2.6	1789	7	US-60-507-511-593	Sequence 593, App
44	37.6	2.6	8591	6	US-10-221-714A-291	Sequence 291, App
45	37.2	2.5	1133	1	PCT-US03-21379-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-457-066-42  
; Sequence 42, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-457-066-42

Query Match	98.0%	Score	1444.8	DB	5	Length	3571
Best Local Similarity	99.4%	Pred. No.	0	Mismatches	8	Indels	1
Matches	1460	Conservative	0	Gaps	1		
QY	2	ACTGAGACACAGAGAGCGCTCTAGGAAAAATTTTGGATGGGATATGTGAAACTA	61				
Db	856	AACCTGAGACACAGAGAGCGCTCTAGGAAAAATTTTGGATGGGATATGTGAAACTA	915				
QY	62	CCCTGGATTCTGCTGCCAGAGCGCGCGAGCGCTTCCACCGCAGCGAGCTTTCCC	121				
Db	916	CCCTGGATTCTGCTGCCAGAGCGCGCGAGCGCTTCCACCGCAGCGAGCTTTCCC	975				
QY	122	CGGGCTGGGCTGAGCGCTTGGAGTCGTCGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	181				
Db	976	C-GGCTGGGCTGAGCGCTTGGAGTCGTCGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	1034				
QY	182	CCCACTGAGCMAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGGCC	241				
Db	1035	CCCACTGAGCMAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGGCC	1094				
QY	242	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACAGTCTCCAGGACA	301				
Db	1095	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACAGTCTCCAGGACA	1154				

302 AGGAACAGAACGAGTGCAGATCCCGCATGAGAGAGTTCTCACTATATCTGGTAATG 361  
1155 AGGAACAGAACGAGTGCAGATCCCGCATGAGAGAGTTCTCACTATATCTGGTAATG 1214  
362 GGAGCATCCACAGCCGAAATTTCTCTACATACGTACCCAAAGAAATATGGTGGTGTGGA 421  
1215 GGAGCATCCACAGCCGAAATTTCTCTACATACGTACCCAAAGAAATATGGTGGTGTGGA 1274  
422 GATTAGTTCAGTAGATGAATAATGTCCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
1275 GATTAGTTCAGTAGATGAATAATGTCCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334  
482 TGGAGATCCAGAGACGATATATCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 541  
1335 TGGAGATCCAGAGACGATATATCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 1394  
542 ATGGAAAGTGTATAGACGCTGGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTTTA 601  
1395 ATGGAAAGTGTATAGACGCTGGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTTTA 1454  
602 AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT 661  
1455 AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT 1514  
662 TCTGCACTCACTACAGTATTATCATGCAAGTCAAGAAACCAAGAGTCTCTCGGTGT 721  
1515 TCTGCACTCACTACAGTATTATCATGCAAGTCAAGAAACCAAGAGTCTCTCGGTGT 1574  
722 TGCCCCCTTCACTTTGTCAATGGAGCTGTCTCAACAAATGTGTGACGCTTCAGTACCT 781  
1575 TGCCCCCTTCACTTTGTCAATGGAGCTGTCTCAACAAATGTGTGACGCTTCAGTACCT 1634  
782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 841  
1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 1694  
842 ACAAGCCAAATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCAAGTGG 901  
1695 ACAGCCAAATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCAAGTGG 1754  
902 TGAATCTGAATCTCTCAAGGAAAGAGTAAATCTTACAGCTGCAACCCCGGAATCTCT 961  
1755 TGAATCTGAATCTCTCAAGGAAAGAGTAAATCTTACAGCTGCAACCCCGGAATCTCT 1814  
962 CAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021  
1815 CAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1874  
1022 TGCTCAAGCGCTGTGGAGGAAATTTGTCCCTGTTGTCTCCATAATTCGAATGTCAAT 1081  
1875 TGCTCAAGCGCTGTGGAGGAAATTTGTCCCTGTTGTCTCCATAATTCGAATGTCAAT 1934  
1082 GTGTCCCAAGTAAGTTTACAAAAGTACCAATGAGTCCCTTCACTGAGACCAAAACTG 1141  
1935 GTGTCCCAAGTAAGTTTACAAAAGTACCAATGAGTCCCTTCACTGAGACCAAAACTG 1994  
1142 GAGTCAAGGATTCGATAAGTCACTCACTGATGTGGCTCTGGAACACACAGAGAAATGTG 1201  
1995 GAGTCAAGGATTCGATAAGTCACTCACTGATGTGGCTCTGGAACACACAGAGAAATGTG 2054  
1202 ACTGTGTGTGTAGAGGAAACGACAGAGGTAACCTGACGCTTTCGTAGCAGCACACGTGAG 1261  
2055 ACTGTGTGTGTAGAGGAAACGACAGAGGTAACCTGACGCTTTCGTAGCAGCACACGTGAG 2114  
1262 CACTGGCAATTCGTGTATCCCCCAACAAGCACTTCATCCCAACAGAGGTTGGCCGAGGG 1321  
2115 CACTGGCAATTCGTGTATCCCCCAACAAGCACTTCATCCCAACAGAGGTTGGCCGAGGG 2174  
1322 CTCTCAGCTGTGATGCTGTATGTTAAAGATCTTACTGTCTCCCAACCAAAATCTCAG 1381  
2175 CTCTCAGCTGTGATGCTGTATGTTAAAGATCTTACTGTCTCCCAACCAAAATCTCAG 2234

1382 TTGTTTGGTTCATAGCCCTTCCCTGCGAGACTTCAAGTGTCTTTCTAAAGACCGAGGC 1441  
2235 TTGTTTGGTTCATAGCCCTTCCCTGCGAGACTTCAAGTGTCTTTCTAAAGACCGAGGC 2294  
1442 ACCAANAGGAGTCAATCACAAGACACTGC 1470  
2295 ACCAAGAGGAGTCAATCACAAGACACTGC 2323

RESULT 2  
US-09-876-813-34  
; Sequence 34, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US/09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US/60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US/60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-876-813-34

Query Match 98.0%; Score 1444.8; DB 5; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGGATTATGTGAAACTA 61  
DB 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGGATTATGTGAAACTA 915  
QY 62 CCTGGGATTTCTGTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGAGCCTTTCCC 121  
DB 916 CCTGGGATTTCTGTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGAGCCTTTCCC 975  
QY 122 CGGGCTGGGCTGAGCCCTTGGAGTCGTCTTCCAGTCCCGCGGAGTGAGCCCTCG 181  
DB 976 C-GGCTGGGCTGAGCCCTTGGAGTCGTCTTCCAGTCCCGCGGAGTGAGCCCTCG 1034  
QY 182 CCCAGTTCAGCCAAATGCTCTCTCGGCTCTCTCTGTGACATCTGCCCTGCCCGGCC 241  
DB 1035 CCCAGTTCAGCCAAATGCTCTCTCGGCTCTCTCTGTGACATCTGCCCTGCCCGGCC 1094  
QY 242 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 301  
DB 1095 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAACGAGTGCAGATCCCGCATGAGAGAGTTGTCACTATATCTGGTAATG 361  
DB 1155 AGGAACAGAACGAGTGCAGATCCCGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214  
QY 362 GGAGCATCCACAGCCGAAATTTCTCTACATACGTACCCAAAGAAATATGGTGGTGTGGA 421  
DB 1215 GGAGCATCCACAGCCGAAATTTCTCTACATACGTACCCAAAGAAATATGGTGGTGTGGA 1274  
QY 422 GATTAGTTCAGTAGATGAATAATGTCCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481



Db 1575 TCCCCCTTCATCTTTGTGATTTGGACCTGCTCAAAATGCTGTGATGCTTCACTAGTACT 1634  
QY 782 TGAAGAGCTGATTCGGTACTTAGAGCCAGATCGATGGCAGTGGACTTGGACAGCTCT 841  
Db 1635 TGAAGAGCTGATTCGGTACTTAGAGCCAGATCGATGGCAGTGGACTTGGACAGCTCT 1694  
QY 842 ACAAGCCACATCGCAGCTTTTGGCAGAGCTTCTCTGATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCACATCGCAGCTTTTGGCAGAGCTTCTCTGATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGGAACTTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGGAACTTCT 1814  
QY 962 CAGTGTCCATAGCGGAAGAGCTAAAGAGCAGATACCAATATCTGGCCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCCATAGCGGAAGAGCTAAAGAGCAGATACCAATATCTGGCCAGGTTGTCTCC 1874  
QY 1022 TGGTCAAGCGCTGGAGGAATTTGGCTGTCTCTCCATATTTGCAATGAATGTCACT 1081  
Db 1875 TGGTCAAGCGCTGGAGGAATTTGGCTGTCTCTCCATATTTGCAATGAATGTCACT 1934  
QY 1082 GTGTCCACAGTAAAGTTACAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAAACTG 1141  
Db 1935 GTGTCCACAGTAAAGTTACAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAAACTG 1994  
QY 1142 GAGTCAAGGATGCAATAGTCACTCACTGATGTGCTCTGGACACACAGGATGTG 1201  
Db 1995 GAGTCAAGGATGCAATAGTCACTCACTGATGTGCTCTGGACACACAGGATGTG 2054  
QY 1202 ACTGTGTGTAGAGAAACGAGGAGGTAACTGAGCTCTCGTAGCAGCACAGTGA 1261  
Db 2055 ACTGTGTGTAGAGAAACGAGGAGGTAACTGAGCTCTCGTAGCAGCACAGTGA 2114  
QY 1262 CACTGCACTTGTGTACCCCAACAGCAACCTTCACTCCACAGGTTGGCCGAGGG 1321  
Db 2115 CACTGCACTTGTGTACCCCAACAGCAACCTTCACTCCACAGGTTGGCCGAGGG 2174  
QY 1322 CTTCTAGCTGCTGATGCTGGCTATGTAAGATCTTACTGCTCCACCAAAATCTCAG 1381  
Db 2175 CTTCTAGCTGCTGATGCTGGCTATGTAAGATCTTACTGCTCCACCAAAATCTCAG 2234  
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGAGGC 2294  
QY 1442 ACCAAGAGGAGTCAATCAAAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCAAAAGCACTGC 2323

RESULT 4  
PCT-US03-26491-58  
; Sequence 58, Application PC/TUS0326491  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT  
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/26491  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 58  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US03-26491-58

Query Match 62.0%; Score 914.2; DB 1; Length 3007;  
Best Local Similarity 83.5%; Pred. No. 6.e-285;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 61  
Db 294 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 353  
QY 62 CCTCGGATTCCTGTCGACAGCGGCGCTTCCACCGCAGCGCAGCTTTTCCC 121  
Db 354 CCTCGGATTCCTGTCGACAGCGGCTCGCGCTTCCACCGCAGCGCAGCTTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCTTTGGAGTGTCTTCCAGTCCCGCGCGAGTGAGCC 177  
Db 414 TGGCGGTGGTGAAGAGAGACTCGGGAGTGTCTTCCAAAGTCCCGCGCTGAGTGAGCT 473  
QY 178 CTCGCCCGAGTCAGCCAAATGTCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCC 237  
Db 474 CTCACCCAGTCAGCCAAATGAGCCTCTTTCGGGCTTCTCTGCTGACATCTGCCCTGGCC 533  
QY 238 GGCCAAAGAACGGGAGTCCGGCTGAGTCCAACTGAGCAGCAAGTTGAGAGCTCTCCAGC 297  
Db 534 GGCAGAGACAGGGAGTCTAGCGGAAATCCAACTGAGTAGTAATTCAGTTTCCAGC 593  
QY 298 GACAAAGAACAGAGCGAGTGCAGATCCCGCATGAGAGATTTCTACTATATCTGGT 357  
Db 594 AACAAAGAACAGAGCGAGTGCAGATCCAGATCTCAGCATGAGAGAAATTTACTGTGTACT 653  
QY 358 AATGGAGCATCCAGCCCGAAGTTTCTCTATACGTACCAAGAAATATGGTCTGGTG 417  
Db 654 AATGGAAGTATTCACAGCCCAAGTTTCTCTATACGTATTCACAAAGAAATACGGTCTGGTA 713  
QY 418 TGGAGATTTAGTTGACATAGTAAATGTCGGATCCAGTGCATCTGATGAGAGATTT 477  
Db 714 TGGAGATTTAGTTGACATAGTAAATGTCGGATCCAGTGCATCTGATGAGAGATTT 773  
QY 478 GGGCTGGAAGATCCAGAGACGATATATCAAGTATGATTTTGTAGAGTTGAGAGGCC 537  
Db 774 GGGCTTGAAGACCCAGAGATGACATATCAAGTATGATTTTGTAGAGTTGAGAGAACCC 833  
QY 538 AGTGTAGAGTGTGTTTAGGACGCTGTGTGTTCTGGACTGTGCCAGAGAGAGAGT 597  
Db 834 AGTGTAGAGTGTGTTTAGGACGCTGTGTGTTCTGGTACTGTACAGAGAAACAGAT 893  
QY 598 TCTAAGAGAAATCATATCAGGATAAGATTTGATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 894 TCTAAGAGAAATCAAATTAGATTTGATCTGATGAGTATTTTCCATCTGAACCA 953  
QY 658 GGATTCCTCATCCACTACAGATATTATCATGCCCAAGTCAAGAAACAGAGTCTTCCG 717  
Db 954 GGTTTCTGCATCCACTACAACTTGTCTGCGCAATTCACAGAAAGCTGTGAGTCTCTCA 1013  
QY 718 GTGTTGCCCTTCTATCTTGTGATTTGGACCTGCTCAACAATCTGTGACTGCTTCCAGT 777  
Db 1014 GTGCTACCCCTTTCAGCTTTGCCACTGAGCTCTTAATTAATGCTATTAATGCTTTAGT 1073  
QY 778 ACCTTGAAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGTGGACTTGGACAGC 837  
Db 1074 ACCTTGAAGAGCTTATTCGATATCTTGAACACAGAGAGTGGCAGTTGGACTTAGAGAT 1133  
QY 838 CTCACAAGCCAAACATGGCAGCTTTTGGCAAGGCTTTCTGTATGGGAAAAAAGCAAA 897  
Db 1134 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAAAATCCAGA 1193  
QY 898 GTGGTGAATCTGAATCTCTCAGGAAGAGGTAAACTCTACAGCTGCGACACCCCGGAC 957  
Db 1194 GTGGTGAATCTGAACCTTCTAACAGAGGAGGTAAAGATTTACAGCTGCGACACCTCGTAA 1253  
QY 958 TTCTCAGTGTCCATAGCGGAAGAGCTTAAAGAGAGACAGATACCATATTTCTGGCCAGGTTGT 1017  
Db 1254 TTCTCAGTGTCCATAGCGGAGAGCTTAAAGAGAGACCGATACCATTTCTGGCCAGGTTGT 1313  
QY 1018 CTCCTGGTCAAGCGCTGTGGAGGAAATGTGCTGTGCTCTCCATTAATTTGCAATGAATGT 1077

Db 1314 CTCCTGGTTAAACGCTGTGGTGGAACTGTGCCCTGTGTCTCCACAATTCGAATGAATGT 1373  
QY 1078 CAGTGTGTCCCAAGTAAAGTTACAAAAGTACATGAGGTCTCTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGCAAGTTACTAAAANAATACCAAGAGTCTCTCAGTTGAGACCAAG 1433  
QY 1138 ACTGGAGTCAAGGATGTCATAGTCACTCAGTATGTGGCTCTGGAAACCAACGAGGAA 1197  
Db 1434 ACCGGTGTGAGGGGATGCAAAATCACTCAGGAGTGGCCCTGGAGCAACCATGAGGAG 1493  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGTAACTGAGCCTTCGTAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTGAGAGGAGACAGGAGGATAGCCGATCACCAACGAGCCTC 1550

RESULT 5  
US-10-648-593-58  
; Sequence 58, Application US/10648593  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT  
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 NP  
; CURRENT APPLICATION NUMBER: US/10/648,593  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 58  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-648-593-58

Query Match 62.0%; Score 914.2; DB 6; Length 3007;  
Best Local Similarity 83.5%; Pred. No. 6.6e-285;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGCGAACTA 61  
Db 294 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGCGAACTA 353  
QY 62 CCTGCGATCTCTGCTGCCAGAGCGGCGCAGCGGCTTCCACCGCAGCGAGCCTTTGCC 121  
Db 354 CCTGCGATCTCTGCTGCCAGAGCAGGCTCGCGGCTTCCACCCAGTCAGCCTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCAAGTCCCGCGCGAGTGAGCC 177  
Db 414 TGGCGGTGTGTGAAGAGACTCGGGAGTGTGCTTCCAAAGTCCCGCGCGTGTGAGTGAGCT 473  
QY 178 CTCGCCCCAGTCAGCCAAATGTCTCTCGGCTCTCTCTGCTGATCATCTGCCCTGGCC 237  
Db 474 CTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTGATCATCTGCCCTGGCC 533  
QY 238 GGCACAAAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGC 297  
Db 534 GGCACAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAATTCAGTTTCCAGC 593  
QY 298 GACAAGAACACAGACCGAGTGAAGATCCCGGATGAGAGGTTGTCTACTATCTGGT 357  
Db 594 AACAAAGAACACAGACCGAGTGAAGATCCCTCAGCATGAGAGATTTACTGTGTCTACT 653  
QY 358 AATGGGAGCATCCACAGCCGGAAGTTTCTCATACGTACCCAGAAATATGGTCTGGTG 417  
Db 654 AATGGAAGTATTCACAGCCCAAGTTTCTCTACTTATTCAGAAATAGGCTTGGTA 713  
QY 418 TGGAGATTAGTTGACGTAGATGAAAATGTGGGATCCAGCTGACATTTGATGAGATTT 477  
Db 714 TGGAGATTAGTACAGTAGAGGAATGATGATGATACACTTACCTTGTGATGAAGATTT 773

QY 478 GGCTCGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 537  
Db 774 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAAGTTGAGAAACC 833  
QY 538 AGTGTGGAAGTCTTTTAGGACGCTGGTGGTCTCTGGGACTGTGCCAGGAAGACAGACT 597  
Db 834 AGTGTGGAAGTCTTTTAGGCGCTGGTGGTCTCTGGTACTGTACCAGAAACAGATT 893  
QY 598 TCTAAAGGAAATCATATCAGGATAAGATTTGTATCTCATGAGTATTTTCCATCTGAACCC 657  
Db 894 TCTAAAGGAAATCAATTAGGATAAGATTTGTATCTCATGATATTTTCTTCTGAACCA 953  
QY 658 GGAATCTGCATCCACTACAGTATATCATGCCCAAGTCAAGAAACCAAGGCTCTTCG 717  
Db 954 GGGTTCTGCATCCACTACAACTTGTCTATGCCCAATTCACAGAAAGTGTGAGTCTTCA 1013  
QY 718 GTCTTGGCCCTTCACTTTGTCTATTGGACCTCTCAACATGCTGTGACTGCTTCACT 777  
Db 1014 GTCTTACCCCTTCACTTTGGCCACTGGACTCTTAATATGCTATTAACCTGCTTTAGT 1073  
QY 778 ACCTTGAAGAGTGTATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC 837  
Db 1074 ACCTTGAAGACCTTATTCGATATCTTGAACGAGAGATGGCAGTTGGACTTAGAAGAT 1133  
QY 838 CTCTAAGCCCAACATGCGAGCTTTTGGGCAAGCTTCTCTGTATGGGAAAAAAGCAAA 897  
Db 1134 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTCTTGTGGAAAGAAATCCAGA 1193  
QY 898 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCGAGAC 957  
Db 1194 GTGGTGAATCTGAACCTTCTTAAACAGAGGAGGTAAAGTATACAGCTGCACACCTCGTAAC 1253  
QY 958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGCCCAGGTTGT 1017  
Db 1254 TTCTCAGTGTCCATAGGAGAGACTTAAAGAGAACCATATACCATTTCTGCCCAGGTTGT 1313  
QY 1018 CTCTGGTCAAGCTGTGTGAGGAAATGTGCTGTGTGTCTTCCATAATTCGAATGAATGT 1077  
Db 1314 CTCTGGTAAACGCTGTGTGGGAACTGTGCTGTGTCTCCACAATTCGAATGAATGT 1373  
QY 1078 CAGTGTGTCCACGTAAAGTTACAAAAAGTACCATGAGTCTTCAAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGCAAGATTAATAAAATATACAGAGTCTTCAAGTTGAGACCAAAG 1433  
QY 1138 ACTGGAGTCAAGGATTCGATAGTCACTCAGTATGTGCTCTGGAACCAACGAGGAA 1197  
Db 1434 ACCGGTGTGAGGGATTCGACAAATCACTACCGAGCTGGGCTTGGAGCAACCATGAGAG 1493  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTTAACTGAGGCTTCTGAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTGAGAGGAGCAGGAGGATAGCCGATCACCAACGAGCCTC 1550

RESULT 6  
US-60-507-511-2084  
; Sequence 2084, Application US/60507511  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI  
; FILE REFERENCE: AM 101081  
; CURRENT APPLICATION NUMBER: US/60/507,511  
; CURRENT FILING DATE: 2003-10-02  
; NUMBER OF SEQ ID NOS: 203623  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2084  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-507-511-2084

Query Match 62.0%; Score 914.2; DB 7; Length 3007;



Best Local Similarity 83.5%; Pred. No. 6.6e-285;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGAAAATTTTGGATGGGATATGTGGAAACTA 61  
Db 294 AACTGGAGACACAGAGAGGGCTCTAGAAAATTTTGGATGGGATATGTGGAAACTA 353  
QY 62 CCCTGCGATTCTCTGCTGCGAGAGCGCGCGAGGGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 354 CCCTGCGATTCTCTGCTGCGAGAGCGCGCGAGGGCTTCCACCGCAGCTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCTTGGAGTGTGCTTCCCGAGTGCCTCCGCGAGTGAGCC 177  
Db 414 TGGCGGTGGTGAAGAGACTCGGGAGTGTGCTTCCCGAGTGCCTCCCGCGAGTGAGCT 473  
QY 178 CTGCCCCCAGTTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGAGCATCTGCCCTGGCC 237  
Db 474 CTACCCCGAGTTCAGCCAAATGAGCCTCTTGGGGTCTCTCTGCTGAGCATCTGCCCTGGCC 533  
QY 238 GGCCAAAGAACGGGGAAGTTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGC 297  
Db 534 GGCCAGAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAATTTCCAGTTTCCAGC 593  
QY 298 GACAAGAAACAGACCGAGTCAAGATCCCGGATCAGAGAGTGTGCATATATCTGGT 357  
Db 594 AACAAAGAAACAGACCGAGTCAAGATCCCGATCAGAGAGTATATATCTGTGTCTACT 653  
QY 358 AATGGGAGATCCACAGCCCGAGTTTCTCATACGTACCCAGAAATATGTCGTCTGGTG 417  
Db 654 AATGGAAGTATCCAGCCCAAGTTTCTCATACTATCCAGAAATATCGTCTTGGTA 713  
QY 418 TGGAGATTAGTGTGAGTAGATGAAAATGTGGGATCCAGCTGACATTTGATGAGATTT 477  
Db 714 TGGAGATTAGTGTGAGTAGAGAAAATGTATGATACAACTTACGTTTGTATGAAAGATTT 773  
QY 478 GGGCTGGAAGATCCAGAGAGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 537  
Db 774 GGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGAGACC 833  
QY 538 AGTATGGAAGTGTGTTAGGACGCTGTGTGGTCTCGGATGTGCGAGGAAGCAGACT 597  
Db 834 AGTATGGAATATATAGGGCGCTGTGTGGTCTGGTACTGTGACGAGGAAGACAGATT 893  
QY 598 TCTAAGGAATCATATCAGGATTAAGATTTGTATCTGATGATATTTTCCATCTGAACCC 657  
Db 894 TCTAAGGAATCAATTAGGATAAGATTTGTATCTGATGATATTTTCTTCTGAACCA 953  
QY 658 GGATTTGCTATCCACTACAGTATTTATCATGCCAAGTCCAGAAACCAAGAGTCTCTCG 717  
Db 954 GGGTTCTGCATCCACTACAAATTTGTATGCAATTTGTATGCAATTTTCAAGAGCTGTGAGTCTTCA 1013  
QY 718 GTGTGCCCCCTTTCATCTTTGTCTATTTGACCTGCTCAACATGCTGTGACTGCTCTCAGT 777  
Db 1014 GTGTACCCCCCTTTCAGCTTTGCCACTGGACTGCTTAATATGCTAATATGCTCTTAGT 1073  
QY 778 ACCTTGAAGAGCTGATTCGGTATCCTAGAGCCAGATCGATGGCAGGTGGACTTCGACAGC 837  
Db 1074 ACCTTGAAGAGCTTATTCGATATCTTGAACAGAGAGATGGCAGTTTGGACTTGAAGAT 1133  
QY 838 CTCTACAGCCCAATCGCAGCTTTTGGGCAAGCTTTCTGTATGAGGAAAAGCAAA 897  
Db 1134 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGTGTTTGAAGAAAATCCAGA 1193  
QY 898 GTGTGTAATCTGAATCTCTCAAGGAAGAGGTAATACTCTACAGCTGCACACCCCGGAAC 957  
Db 1194 GTGTGGATCTGAACCTTCTAACAGAGAGGATAGATTTATACGTGCAACCTCTGTAC 1253  
QY 958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGT 1017  
Db 1254 TTCTCAGTGTCCATAAAGGAAGAACTAAAGAGAACCGATACCAATTTCTGCCAGGTGT 1313  
QY 1018 CTCTGCTCAGCGCTGTGGAGAAATTTGTCCTGTTGTCTCCATATTTGCAATGAATGT 1077

Db 1314 CTCTGTTTAAACGCTGTGTTGGGAACACTGTGCTGTTGTCTCCAAATTTGCAATGAATGT 1373  
QY 1078 CAGTGTGTCCACGTAAGTTTACAAAAGTACCATGAGTTCCTTTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGCAAAAGTTTACTTAAAAAATACCACGAGGTCTTTCAGTTGAGACCAAA 1433  
QY 1138 ACTGGAGTCAAGGATTTGCAATAGTCACTCACTGATGTGGCTTGGAAACCAACGAGGAA 1197  
Db 1434 ACCGTGTCAAGGATTTGCAAAATCACTCACCAGCTGGCCCTGGAGCACCATGAGGAG 1493  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGAGGGTAACTGACAGCCTTGTAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTAGAGGAGCACAGGAGTAGCCGATCATCACCACGAGCTC 1550

RESULT 7  
US-60-487-610-231  
; Sequence 231, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; FILE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-487-610-231

Query Match 62.0%; Score 913.8; DB 7; Length 3007;  
Best Local Similarity 83.5%; Pred. No. 9e-285;  
Matches 1049; Conservative 1; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGGGCTCTAGAAAATTTTGGATGGGATATGTGGAAACTA 61  
Db 294 AACTGGAGACACAGAGGGCTCTAGAAAATTTTGGATGGGATATGTGGAAACTA 353  
QY 62 CCCTGCGATTCTCTGCTGCGAGAGCGCGCGAGGGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 354 CCCTGCGATTCTCTGCTGCGAGAGCGCGCGAGGGCTTCCACCGCAGCTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTGCCTCCGCGAGTGAGCC 177  
Db 414 TGGCGGTGGTGAAGAGACTCGGGAGTGTGCTTCCCGAGTGCCTCCCGCGAGTGAGCT 473  
QY 178 CTGCCCCCAGTTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGAGCATCTGCCCTGGCC 237  
Db 474 CTACCCCGAGTTCAGCCAAATGAGCCTCTTGGGGTCTCTCTGCTGAGCATCTGCCCTGGCC 533  
QY 238 GGCCAAAGAACGGGGAAGTTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGC 297  
Db 534 GGCCAGAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAATTTCCAGTTTCCAGC 593  
QY 298 GACAAGAAACAGACCGAGTCAAGATCCCGGATCAGAGAGTGTGCATATATCTGGT 357  
Db 594 AACAAAGAAACAGACCGAGTCAAGATCCCGATCAGAGAGTATATATCTGTGTCTACT 653  
QY 358 AATGGGAGATCCACAGCCCGAGTTTCTCATACGTACCCAGAAATATGTCGTCTGGTG 417  
Db 654 AATGGAAGTATCCAGCCCAAGTTTCTCATACTATCCAGAAATATCGTCTTGGTA 713  
QY 418 TGGAGATTAGTGTGAGTAGATGAAAATGTGGGATCCAGCTGACATTTGATGAGATTT 477  
Db 714 TGGAGATTAGTGTGAGTAGAGAAAATGTATGATACAACTTACGTTTGTATGAAAGATTT 773  
QY 478 GGGCTGGAAGATCCAGAGAGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 537

Db 774 GGCTTTGAAGACCCAGAGATGATATGATTTTGTAGAAGTTGAGGAACCC 833  
QY 538 AGTGATGGAAGTGTCTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGGAAGCAGACT 597  
Db 834 AGTGATGGAACATATTTAGGCGCTGGTGTGGTCTGGTACTGTACCGAGGAACAGATT 893  
QY 598 TCTAAAGGAATCATATCAGGATAAGATTGTGTATCTGTATGTAGTATTTTCCATCTGAACCC 657  
Db 894 TCTAAAGGAATCAAAATTAGATAAGATTGTGTATCTGTATGTAGTATTTTCCATCTGAACCA 953  
QY 658 GGATCTGCATCCACTACAGTATATCATGSCCAAGTACAGAAACACAGAGTCTCTCG 717  
Db 954 GGTTCTGCATCCACTACAACTGTATGCCCAATTCACGAAGCTGTGAGTCTCTTCA 1013  
QY 718 GTTTGCCCTTCATCTTTGTCAATGGACCTGCTCAACAAATGCTGTGACTGCTTCAGT 777  
Db 1014 GTGTACCCCTTCAGCTTTGGCACTGGACCTGCTTAAATGCTATACTGCTTTAGT 1073  
QY 778 ACCTTGAAGAGCTGATTTGGTACCTTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGC 837  
Db 1074 ACCTTGAAGAGCTTATTCGATATCTTGAACCGAGAGATGGCAGTTGGACTTTAGAAGAT 1133  
QY 838 CTCTAAGCAACATGCGCAGCTTTTGGGCAAGCTTTCTGTATGGGAAAAAGCAAA 897  
Db 1134 CTATATAGGCAACTTTGGCACTTTCTTGGCAAGCTTTTGTTTTGGAGAAATCCAGA 1193  
QY 898 GTGGTGAATCTGAATCTCTCTCAAGGAAGGTAAATCTCTACAGCTGCACACCCCGAAC 957  
Db 1194 GTGGTGAATCTGAATCTCTCTCAAGGAAGGTAAATCTCTACAGCTGCACACCCCGAAC 1253  
QY 958 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1017  
Db 1254 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1313  
QY 1018 CTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1077  
Db 1314 CTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1373  
QY 1078 CAGTGTGTCCAGTAAAGTTACAAAAGTACATAGAGTCTTTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCAGCAAGTTACTAAAAAATACCAAGAGTCTTTCAGTTGAGACCAAA 1433  
QY 1138 ACTGGAGTCAAGGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197  
Db 1434 ACCGGTGTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493  
QY 1198 TGTGACTGTGTGTAGAGGAACGAGGAGGTAACTGAGGCTTCTGAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTAGAGGAACGAGGAGGTAACTGAGGCTTCTGAGCAGCAC 1550

## RESULT 8

US-60-485-450-137  
; Sequence 137, Application US/60485450  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: CHANG, Sheng-yung  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001470  
; CURRENT APPLICATION NUMBER: US/60/485,450  
; CURRENT FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 47859  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 137  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-485-450-137

Query Match

62.0%; Score 913.8; DB 7; Length 3007;

Best Local Similarity 83.5%; Pred. No. 9e-285;  
Matches 1049; Conservative 1; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 294 AACTGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 353  
QY 62 CCCTGGATTTCTGCTGCCAGAGCCGGCAGGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 354 CCCTGGATTTCTGCTGCCAGAGCCGGCAGGCTTCCACCGCAGCGAGCTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCTTGGAGTCTGCTTCCCAGTGGCCGCGAGTGAAC 177  
Db 414 TGGCGGTGGTGAAGAGACTCGGGAGTCTGCTTCCAAAGTGGCCGCGAGTGAAC 473  
QY 178 CTGCCCCCAGTCAAGCAATGCTCTCTCGGCTCTCTCTGCTGCTGCTGCTGCTGCTG 237  
Db 474 CTGCCCCCAGTCAAGCAATGAGCTCTCTCTCGGCTCTCTCTGCTGCTGCTGCTGCTG 533  
QY 238 GGCCAAAGAAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTTCCAGC 297  
Db 534 GGCCAGAGACAGGGAGCTCAGGCGGAATCCAACTGAGTAGTAAATTTCCAGTTTCCAGC 593  
QY 298 GACAAGGAACAGAACCGAGTGAAGATCCCGGATGAGAGAGTTGTCTATATCTGCT 357  
Db 594 AACAGGAACAGAACCGAGTGAAGATCCCTCAGCATGAGAGAAATTTACTGTGCTACT 653  
QY 358 AATGGAGAGCATCCACAGCCGGAAGTTTCTCATAGCTACCAAGAAATATGGTCTGCTG 417  
Db 654 AATGGAGATTTTCCAGAGCCCAAGTTTCTCATATCTTATCCAAAGAAATAGCGTCTGTA 713  
QY 418 TGGAGATTTAGTTGCTGAGTAGTAAATTTGTCGGATCCAGCTGACATTTTGTATGAGAGATT 477  
Db 714 TGGAGATTTAGTTGCTGAGTAGTAAATTTGTCGGATCCAGCTGACATTTTGTATGAGAGATT 773  
QY 478 GGCTGGAAGATCCAGAGAGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 537  
Db 774 GGCTTGAAGACCCAGAGATGATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 833  
QY 538 AGTGATGGAAGTGTGTTAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597  
Db 834 AGTGATGGAAGTGTGTTAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 893  
QY 598 TCTAAAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCC 657  
Db 894 TCTAAAGGAATCAAATTTAGATAAGATTTGTATCTGATGAATATTTTCTTCTGAAACCA 953  
QY 658 GGATTTCTGATCCACTACAGTATATCATGCCCCAGTCAAGAAACCAAGTCTCTCG 717  
Db 954 GGCTTCTGATCCACTACAGTATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 1013  
QY 718 GTGTGCCCCCTTCATCTTTGTCTATTGGACCTGCTCAACAAATGCTGCTGCTTCCAGT 777  
Db 1014 GTGTGCCCCCTTCATCTTTGTCTATTGGACCTGCTCAACAAATGCTGCTTCCAGT 1073  
QY 778 ACCTTGAAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGC 837  
Db 1074 ACCTTGAAGAGCTTATTCGATATCTTTGAACACAGAGATGCGCAGTTGGACTTTAGAAGAT 1133  
QY 838 CTCTAAGAGCCACATGCGCAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAGCAAA 897  
Db 1134 CTATATAGGCCCACTTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAGAAAAATCCAGA 1193  
QY 898 GTGGTGAATCTGAATCTCTCTCAAGGAAGGTAAATCTCTACAGCTGCACACCCCGAAC 957  
Db 1194 GTGGTGAATCTGAATCTCTCTCAAGGAAGGTAAATCTCTACAGCTGCACACCCCGAAC 1253  
QY 958 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1017  
Db 1254 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1313  
QY 1018 CTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGT 1077

Db 1314 CTCCTGTTAAACGCTGTGGGAACTGTGCTGTTGTTCTCCACAATTGCAATGAATGT 1373  
Qy 1078 CAGTGTCTCCACTAAAGTTACAAAAGATACCATGAGGTCTTTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGAAAGTTACTAAAAAATACACGAGGTCCCTTCAGTTGAGACCAAG 1433  
Qy 1138 ACTGAGTCAAGGATTGCAATGCACTCACTGATGTGGCTCTGGAACACACGAGGAA 1197  
Db 1434 ACCGTGTGAGGATTGCAAAATCACTACCGAGGTGGCCCTGGAGCACCATTGAGGAG 1493  
Qy 1198 TGTGACTGTGTGTAGAGAAACGAGAGGGTAACTGCGACCTTCGTAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTGAGAGGAGCAGAGGGATAGCGCATCCACCACGACGCTC 1550

## RESULT 9

US-09-830-320A-8  
; Sequence 8, Application US/09830320A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: GUEGLER, Karl J.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: AU-YOUNG, Janice K.  
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES  
; FILE REFERENCE: PP-0627 USN  
; CURRENT APPLICATION NUMBER: US/09/830,320A  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: PCT/US99/25458  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: US 60/183,024  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: US 60/155,216  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/172,233  
; PRIOR FILING DATE: 1999-05-17  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PERL Program  
; SEQ ID NO 8  
; LENGTH: 2779  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No.: 4163378CB1

US-09-830-320A-8  
Query Match 61.9%; Score 912.6; DB 5; Length 2779;  
Best Local Similarity 83.5%; Pred. No. 2.1e-284;  
Matches 1049; Conservative 0; Mismatches 204; Indels 4; Gaps 1;  
Qy 2 ACCTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 60 AACTGGAGACACAGAGGGCTCTAGGAAAAGTTTGGATGGGATTTATGTGAAACTA 119  
Qy 62 CCCTGCGATTCTCTGCTGCAGAGCCGCGCCAGCGCTTCCACCGCAGCGAGCCTTTCCC 121  
Db 120 CCCTGCGATTCTCTGCTGCAGAGCGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCC 179  
Qy 122 CGG----GCTGGGTGAGCCTTGAGTGTGTCGCTTCCCAAGTGCAGCGCGAGTGAGCC 177  
Db 180 TGGCGGTGGTGAAGAGACTCGGAGTGTGCTGCTTCCAAAGTGCAGCGCGGTGAGGCT 239  
Qy 178 CTCGCCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTGCTGACATCTGCCCTGGCC 237  
Db 240 CTCACCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTGACATCTGCCCTGGCC 299  
Qy 238 GGCCAAAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGC 297  
Db 300 GGCCAGAGACAGGGGACTCAGCGGAATCCAACTGAGTAGTAATCCAGTTTTCAGC 359

## RESULT 10

US-09-457-066-1  
; Sequence 1, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.

Qy 298 GACAAGGAACAGAACGAGTGCAGATCCCGGCATGAGAGTGTGTCACTATATCTGGT 357  
Db 360 AACAGGAACAGTACGAGGTACAGATCCTCAGCATGAGAGATTTATCTGTCTACT 419  
Qy 358 AATGGGAGATCCACAGCCCGAAGTTTCTCATACGTACCCAGAAATATGGTGTGTG 417  
Db 420 AATGGAAGTATTCACAGCCCAAGGTTTCTCATACTTTATCCAGAAATACGGTCTGTGA 479  
Qy 418 TGGAGATTAGTTGAGTAGATGAATGTGCGGATCCAGCTGACATTTGATGAGAGATT 477  
Db 480 TGGAGATTAGTAGCAGTAGAGGAAATGTATGGGATCAAACTTACGTTTGTATGAAGATT 539  
Qy 478 GGGCTCGAAGATCCAGAAAGCAGATATATGCAAGTATGATTTTGTAGAGTTGAGAGGCC 537  
Db 540 GGGCTTCAGACCCAGAAAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGGAAACC 599  
Qy 538 AGTATGGAAGTGTTTAGGACGCTGTGTGGTCTGTGGACTGTGCCAGGAAAGCAGACT 597  
Db 600 AGTATGGAACATAATATAGGGCGCTGTGTGGTCTGTGGTCTGTACACGAGGAAACAGATT 659  
Qy 598 TCTAAAGGAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 660 TCTAAAGGAATCAAAATGAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCA 719  
Qy 658 GGATTCTGCATCCACTACAGTATTATCATGCCACAAGTCCAGAAACCCAGAGTCTCTCG 717  
Db 720 GGGTCTCGATCCACTACACATTTGTCTATGCCACAATTCACAGAAAGCTGTGAGTCTTCA 779  
Qy 718 GTGTGCCCCCTTCATCTTTGTGATGGAACCTGTCTCAAAATGCTGTGACTGCTTCACT 777  
Db 780 GTGTACCCCCCTTCAGCTTTGCCACTGACCTGTCTTAATATGCTATAACTGCTTTAGT 839  
Qy 778 ACCTTGAAGAGCTGATTTCGATCTCTAGAGCCAGATCGATGCGAGTGGAGCTTGACAGC 837  
Db 840 ACCTTGAAGAGCTTATTCGATATCTTGAACAGAGAGAGTGGAGTTGGACTTTAGAAGAT 899  
Qy 838 CTCTACAAGCCAAATCGCAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAA 897  
Db 900 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGGAAAGAAATCCAGA 959  
Qy 898 GTGTGAAATCTGAATCTCTCAAGGAAGAGTAAATCTCTACAGCTGCACACCCCGGAAC 957  
Db 960 GTGTGGATCTGAACCTTCTAAACAGAGAGAGTAAAGATTTATACAGCTGCACACCTCGTAAC 1019  
Qy 958 TTCTCAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGSCCAGGTGT 1017  
Db 1020 TTCTCAGTGTCCATAGGAGAGAACTAAAGAAACCGATACCATTTCTGSCCAGGTGT 1079  
Qy 1018 CTCTGTGTCAAGCGCTGTGGAGGAAATTTGTGCTTGTGTCTCTCAATAATTTGCAATGAATGT 1077  
Db 1080 CTCTGTGTAAACGCTGTGTGGGAACTGTGCTTGTGTCTCTCAATAATTTGCAATGAATGT 1139  
Qy 1078 CAGTGTCTCCACCTAAAGTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAA 1137  
Db 1140 CAATGTGTCCCAAGAAAGTTACTAAAAAATACCAAGAGTCTTTCAGTTGAGACCAAAAG 1199  
Qy 1138 ACTGAGTCAAGGATTGCAATGCACTCACTCATGATGTGGCTCTGGAACACACAGAGAA 1197  
Db 1200 ACCGTTGTAGGGGATTTGCACAAATCACTACCGAGCTGGCCCTTGAGACCATGAGAG 1259  
Qy 1198 TGTGACTGTGTGTAGAGGAAACGAGAGGGTAACTGACAGCCTTCTGTAGCAGCAC 1254  
Db 1260 TGTGACTGTGTGTGACAGAGGAGCAGAGGAGTAGCGCATCACCCACGACGCTC 1316

## RESULT 10

US-09-457-066-1  
; Sequence 1, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.

```
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-457-066--1

Query Match      59.6%; Score 878.8; DB 5; Length 1760;
Best Local Similarity 83.4%; Pred. No. 1.5e-273;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGGAACCTACCTCGGATTTCTCTGCGAGCGCGCGAGCGCGCTTCCACCGC 106
Db 1 ATTATGTGGAACCTACCTCGGATTTCTCTGCGAGCGCGCGAGCGCGCTTCCACCGC 60

QY 107 AGCGGAGCCTTTCCCGG-----GCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTGC 162
Db 61 AGTGAGCCTTCCCTCGGCGGTGGTGAAGAGACTCGGAGTCTGCTTCCAAAGTGC 120

QY 163 CGCGGAGTGAGCCTCGCGCCAGTCAGCAATGCTCTCTCGGCGCTTCCCTGCTG 222
Db 121 CGCGGTGAGTGAGCTCTCACCCAGTCAGCAATGAGCTCTTGGGCTTCTCTGCTG 180

QY 223 ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 282
Db 181 ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 283 TTGCAGCTCTCCAGCGACAGGACAGAACCGAGTCAAGTCCCGGATGAGAGTT 342
Db 241 TTCCAGTTTCCAGCAACAGGACAGAACCGAGTCAAGTCCCGGATGAGAGTT 300

QY 343 GTCACTATATCTGTAATGGAGCATCCACAGCCGGAAGTTTCTCATAGTACCCCAAGA 402
Db 301 ATTACTGTGCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATACTTATCCAAGA 360

QY 403 AATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
Db 361 AATACGGTCTTGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAACTTACG 420

QY 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTA 522
Db 421 TTTGATGAAGATTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATTTGTA 480

QY 523 GAAGTTGAGAGCCCGAGTGTAGTGAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTG 582
Db 481 GAAGTTGAGAACCCAGTGTAGTGAAGTGTATATAGGCGCTGCTGCTGCTGCTGCTGTA 540

QY 583 CCAGGAACAGAGCTTCTAAGAGAAATCATATCAGGATAGATTGCTATCTGATGAGTAT 642
Db 541 CCAGGAACAGAGTTCTAAGAGAAATCAAATTAGGATAAGATTGTTATCTGATGAATAT 600

QY 643 TTTCCATCTGAACCCGGAATTTCTGCATCCACTACAGTATTATCATGCCAACAGTACAGAA 702
Db 601 TTTCTCTGAACACAGGTTTCTGCATCCACTACAGATTGCTATGCCAACATTCACAGAA 660

QY 703 ACCAGAGTCTTCCGGTGTGCCCCCTTCATCTTTGTCATGACCTGCTCAACAATGCT 762
Db 661 GCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCACTGACCTGCTTAATAATGCT 720

QY 763 GTGACTGCTCTTACGTACCTTGGAGAGCTGATTCGTTACCTAGAGCCAGATCATGCGC 822
Db 1 ATTATGTGGAACCTACCTCGGATTTCTCTGCGAGCGCGCTGCGGCTTCCACCGC 60

Db 721 ATAACTGCGCTTTAGTACCTTGGGAAGACCTTTATTCGATATCTTGAAACAGAGATGCGCAG 780
QY 823 GTGGACTTTGGACAGCCTCTACAAGCCCAACATAGCGAGCTTTTGGCAAGGCTTTCTCTGTAT 882
Db 781 TTGGACTTTAGAAGATCTATATAGGCCCACTTTGGCAACTTTTGGCAAGGCTTTTGTGTTTT 840
QY 883 GGGAAAAAAGCAAGTGTGGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGC 942
Db 841 GGAAGAAAAATCCAGAGTGTGGATCTGAACCTTTCTAACAGAGAGGAGTAAAGATTATACAGC 900
QY 943 TGCACACCCCGGAACCTTCTCAGTCTCCATACGGGAGAGCTAAAGAGACAGATACCATA 1002
Db 901 TGCACACCTCGTAACCTTCTCAGTCTCCATAGGGAAGAACTAAAGAGAACCGATACCATT 960
QY 1003 TTCTGCGCAGTGTCTCTCTGGTCAAGCGCTGTGGAGGAAATTTGTGCTTGTCTCCAT 1062
Db 961 TTCTGCGCAGTGTCTCTCTGGTCAAGCGCTGTGGGAACTGTGCTTGTCTCTCCAC 1020
QY 1063 AATTGCAATGAATGTAGTGTGCTCCCAAGTAAATTTACAAAAAGTACCATGAGGTCTT 1122
Db 1021 AATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCACGAGGTCTT 1080
QY 1123 CAGTTGAGACCAAAACTGAGTCAAGGATTCGATAGTCACTCACTGATGTGGCTCTG 1182
Db 1081 CAGTTGAGACCAAAAGCCGCTGTCAGGGGATTCGCAAAATCACTCACCGAGCTGGCCCTG 1140
QY 1183 GAACACACAGGAAATGTGACTGTGTGTAGAGGAAACGACGAGGAGTAACTGCAGCCT 1242
Db 1141 GAGCACCATGAGGAGTGTGACTGTGTGTGACAGGGAGACAGGAGGATAGCCGATCAC 1200
QY 1243 TCCTAGCAGCAC 1254
Db 1201 CACCAGCAGCTC 1212

RESULT 11
US-09-876-813-32
; Sequence 32, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-876-813-32

Query Match      59.6%; Score 878.8; DB 5; Length 1760;
Best Local Similarity 83.4%; Pred. No. 1.5e-273;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGGAACCTACCTCGGATTTCTCTGCGAGCGCGCGAGCGCGCTTCCACCGC 106
Db 1 ATTATGTGGAACCTACCTCGGATTTCTCTGCGAGCGCGCGAGCGCGCTTCCACCGC 60
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109 Db |||||
110 61 AGTGCAGCTTCCCTGGCGGTGGTGAAGAGACTCGGAGTGGTCTTCCAAAGTGCC 120
111 |||||
112 Qy |||||
113 163 CGCGGAGTGAGCCTTCGCCCGCAGTCAAGCAAAATGCTCTCTCGGCGCTTCTCTGCTG 222
114 |||||
115 Db |||||
116 121 CGCGGTGAGTGAGTCTTCAACCCAGTCAAGCAAAATGAGCCTTCTCGGCGTCTCTGCTG 180
117 |||||
118 Qy |||||
119 223 ACATCTGCTGCTGGCGGCAAGAAACGGGACTCGGCTGAGTCCCAACCTGAGCAGCAAG 282
120 |||||
121 Db |||||
122 181 ACATCTGCTGCTGGCGGCAAGAAACGGGACTCGGCGGAATCCAACTGAGTAGTAAA 240
123 |||||
124 Qy |||||
125 283 TTGCAGCTCTCCAGCAACAAGGAACAGAACGGAGTCAAGATCCCGGCGATGAGAGATT 342
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127 Db |||||
128 241 TTCCAGTTTCCAGCAACAAGGAACAGAACGGAGTCAAGATCTCAGCATGAGAGATT 300
129 |||||
130 Qy |||||
131 343 GTCACTATATCTGGTAATGGGAGCATCCACAGCCCGAAGTTTCTCTACGTACCCCAAGA 402
132 |||||
133 Db |||||
134 301 ATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTCATCTTATCCAGA 360
135 |||||
136 Qy |||||
137 403 AATATGCTGCTGGTGGAGATTAGTTGCAGTAGATAAAATGTCGGATCCAGCTGACA 462
138 |||||
139 Db |||||
140 361 AATACGCTTGTGTGAGATAGTAGTAGCAGTAGAGAAATGATGATGATACACTTACG 420
141 |||||
142 Qy |||||
143 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAGACATATATGCAAGTAGATGATTTTGTGA 522
144 |||||
145 Db |||||
146 421 TTTGATGAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGATTTTGTGA 480
147 |||||
148 Qy |||||
149 523 GAAGTTGAGAGCCAGTGTAGTGAAGTGTGTTAGGACGCTGGTGGTCTTGGAGCTGTG 582
150 |||||
151 Db |||||
152 481 GAAGTTGAGAGCCAGTGTAGTGAAGTGTGTTAGGCGCTGGTGGTCTTGGTACTGTGA 540
153 |||||
154 Qy |||||
155 583 CCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAAGATTGTTGATCTGATGAGTAT 642
156 |||||
157 Db |||||
158 541 CCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAAGATTGTTGATCTGATGAGTAT 600
159 |||||
160 Qy |||||
161 643 TTTCCATCTGAACCCGAGTTCTGCATCCATACAGTATTATATGCGCACAAAGTCAAGAA 702
162 |||||
163 Db |||||
164 601 TTTCCCTTCTGAACCCGAGTTCTGCATCCATACAGTATTATGCGCACAAATTCACAGAA 660
165 |||||
166 Qy |||||
167 703 ACCACGAGTCTTCGCTGTTGCCCTTCTATCTTTGTCATTGGACCTGCTCAACAATGCT 762
168 |||||
169 Db |||||
170 661 GCTGTGAGTCTTCAGTGCTACCCCTTTCAGCTTTGCTGCTGAGCTGCTTAAATATGCT 720
171 |||||
172 Qy |||||
173 763 GTGACTGCTTTCAGTACCTTTGGAAGAGCTGATTCGCTTACCTAGAGCCAGATCGATGGCAG 822
174 |||||
175 Db |||||
176 721 ATAATGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACCCAGAGATGGCAG 780
177 |||||
178 Qy |||||
179 823 GTGGAATGGAAGCTCTTACAGGCAACATGGCAGCTTTTGGCAAGGCTTTCCTGTAT 882
180 |||||
181 Db |||||
182 781 TTGGAATGGAAGCTCTTATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTT 840
183 |||||
184 Qy |||||
185 883 GGGAAAAAGCAAGTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGC 942
186 |||||
187 Db |||||
188 841 GGAAGAAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGTGAAGTATATACG 900
189 |||||
190 Qy |||||
191 943 TGCACACCCCGGAATTTCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATA 1002
192 |||||
193 Db |||||
194 901 TGCACACCTCGTAATCTTCTCAGTGTCCATTAAGGGAAGAACTTAAAGAGAACCGATACCATT 960
195 |||||
196 Qy |||||
197 1003 TTTGGCCAGGTTGTCTCTGCTGCTCAAGGCTGTGGAGAAATGTTGCTGTGCTGCTCAT 1062
198 |||||
199 Db |||||
200 961 TTTGGCCAGGTTGTCTCTGCTGCTTAAACGCTGTGGTGGAACTGTGCTGTGCTCTCCAC 1020
201 |||||
202 Qy |||||
203 1063 AATTGCAATGAATGCTGCTGCTGCTTAAAGTGTACAAAAGTACCATGAGTCCCTT 1122
204 |||||
205 Db |||||
206 1021 AATTGCAATGAATGCTGCTGCTGCTTAAAGTGTACAAAAGTACCATGAGTCCCTT 1080
207 |||||
208 Qy |||||
209 1123 CAGTTGAGACCAAAAATCGGAGTCAAGGAGTTCATTAAGTCACTCACTGATGTGGCTGTG 1182
210 |||||
211 Db |||||
212 1081 CAGTTGAGACCAAAAATCGGAGTCAAGGAGTTCATTAAGTCACTCACTGATGTGGCTGTG 1140
213 |||||
214 Qy |||||
215 1183 GAACACCAAGGAATGTGACTGTGTGTGTAGAGAAACCGAGAGGGTAACTGACGCT 1242
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1141 GAGCACCATTGAGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGGATAGCCGATCAC 1200
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1144 1243 TCGTAGCAGCAC 1254
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1146 Db |||||
1147 1201 CACCAGCAGCTC 1212
1148 |||||
1149 RESULT 12
1150 US-10-664-432-1
1151 ; Sequence 1, Application US/10664432
1152 ; GENERAL INFORMATION:
1153 ; APPLICANT: Hart, Charles E.
1154 ; APPLICANT: Gilbertson, Debra G.
1155 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
1156 ; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
1157 ; FILE REFERENCES: 00-12
1158 ; CURRENT APPLICATION NUMBER: US/10/664,432
1159 ; CURRENT FILING DATE: 2003-09-19
1160 ; NUMBER OF SEQ ID NOS: 5
1161 ; SOFTWARE: FastSeq for Windows Version 3.0
1162 ; SEQ ID NO 1
1163 ; LENGTH: 1760
1164 ; TYPE: DNA
1165 ; ORGANISM: Homo sapiens
1166 ; FEATURE:
1167 ; NAME/KEY: CDS
1168 ; LOCATION: (154)...(1191)
1169 US-10-664-432-1
1170
1171 Query Match 59.6%; Score 878.8; DB 6; Length 1760;
1172 Best Local Similarity 83.4%; Pred. No. 1.5e-273;
1173 Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;
1174
1175 Qy 47 ATTATGTGAAAATACCTCTCGGATCTCTCTGTCAGAGCGGCGCAGCGCTTCCACGCG 106
1176 Db 1 ATTATGTGAAAATACCTCTCGGATCTCTCTGTCAGAGCAGGCTCGGCGCTTCCACGCC 60
1177 Qy 107 AGCGAGCCTTTCCCGG----GCTGGCTGAGCCTTGGAGTGTGCTTCCCGAGTGCC 162
1178 Db 61 AGTGCAGCCTTCCCTGGCGGTGGTGAAGAGACTCGGAGTGTGCTTCCAAAGTGCC 120
1179 Qy 163 CGCGCGAGTGAGCCTTCGCCCGCAGTCAGCAAAATGCTCTCTCTCGGCGCTTCTCTGCTG 222
1180 Db 121 CGCGGTGAGTGAGTCTCTACCCCAAGTCAAGCAAAATGAGCCTTCTCGGCGCTTCTCTGCTG 180
1181 Qy 223 ACATCTGCTGCTGGCGGCAAGAAACGGGACTCGGCTGAGTCCCAACCTGAGCAGCAAG 282
1182 Db 181 ACATCTGCTGCTGGCGGCAAGAAACGGGACTCGGCGGAATCCAACTGAGTAGTAAA 240
1183 Qy 283 TTGCAGCTCTCCAGCAACAAGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGATT 342
1184 Db 241 TTCCAGTTTCCAGCAACAAGGAACAGAACGGAGTGAAGATCTCAGCATGAGAGATT 300
1185 Qy 343 GTCACTATATCTGGTAATGGGAGCATCCACAGCCCGAAGTTTCTCTACGTACCCCAAGA 402
1186 Db 301 ATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTCATCTTATCCAGA 360
1187 Qy 403 AATATGCTGCTGGTGGAGATTAGTTGCAGTAGATAAAATGTCGGATCCAGCTGACA 462
1188 Db 361 AATACGCTTGTGTGAGATTAGTAGCAGTAGAGAAATGATGATGATACACTTACG 420
1189 Qy 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAGACATATATGCAAGTAGATGATTTTGTGA 522
1190 Db 421 TTTGATGAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGATTTTGTGA 480
1191 Qy 523 GAAGTTGAGAGCCAGTGTAGTGAAGTGTGTTAGGACGCTGGTGGTCTTGGAGCTGTG 582
1192 Db 481 GAAGTTGAGGAAACCCAGTGTATGAACTATATATTAGGCGCTGGTGGTCTGCTGACTGTGA 540
1193 Qy 583 CCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAAGATTGTTGATCTGATGAGTAT 642
1194 Db 541 CCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAAGATTGTTGATCTGATGAGTAT 600
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Db 121 GTACAAGATCCTAGCATGAGAGAAATTATTACTGTGTCTACTAATGGAAAGTATTTCACAGC 180  
Qy 376 CCGAAGTTTTCCTCATACGTACCCAGAAATATGGTGTGTGGAGATTAGTTGCCAGTA 435  
Db 181 CCAAGTTTCTCTCATACTTATCCAAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTA 240  
Qy 436 GATGAAATATGGCGGATCCAGCTGACATTTGATGAGAGATTGGGCTGGAAAGATCCAGAA 495  
Db 241 GAGGAAATATGATGGATACAACTTACGTTTGTGAAAGATTGGGCTTGAAGACCCAGAA 300  
Qy 496 GACGATATATCAAGTATGATTTTGTAGAACTTGGAGGCCAGTGTGGAGTGGTGTTTTA 555  
Db 301 GATGACATATCAAGTATGATTTTGTAGAACTTGGAGAACCCAGTGTGGAACTATATTA 360  
Qy 556 GGACGCTGGTGTGGTCTTGGGACTGTGCCAGGAAAGCAGACTTCTAAAGGAAATCATATC 615  
Db 361 GGGGCTGGTGTGTCTGTGTACTGTACCAGGAAACAGATTCTTAAGGAAATCAAATT 420  
Qy 616 AGGATAAGATTGTATCTGTATGAGTATTTTCCATCTGAAACCGGATTTCTGCATCCACTAC 675  
Db 421 AGGATAAGATTGTATCTGTATGAGTATTTTCCATCTGAAACCGGATTTCTGCATCCACTAC 480  
Qy 676 AGTATTATCATGCCACAAAGTCACAGAAACACAGAGTCCCTCGGTGTGGCCCTTCATCT 735  
Db 481 AACATTGTATGCCACAAATTCACAGAGCTGTGAGTCCCTTCAGTGTACCCCTTCAGCT 540  
Qy 736 TTGTCAATTGGACCTGTCTCAACAATGCTGTGACTGCTTCAGTACCTTGGAAAGAGCTGATT 795  
Db 541 TTGCCACTGGACCTGTCTTAATAATGCTATAACTGCCCTTTAGTACCTTGGAAAGACCTTATT 600  
Qy 796 GGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCTACAAGCCAAACATGG 855  
Db 601 CGATATCTTGAACACAGAGAGATGGCAGTTGGACTTGAAGATCTATATAGGCCAACTTGG 660  
Qy 856 CAGCTTTTGGCAAGGCTTTCTCTGTATGGGAAAAAAGCAAAGTGGTGAAT 906  
Db 661 CACTTCTTGGCAAGGCTTTGTTTGGAGAAAAATCCAGAGGAGATAT 711

Search completed: November 26, 2003, 09:11:10  
Job time : 275.739 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:39:26 ; Search time 2150.81 Seconds  
(without alignments)  
16656.442 Million cell updates/sec

Title: US-09-852-209A-6

Perfect score: 1474

Sequence: 1 caccctggagacacagaag.....aatcacaaagcactgcacccg 1474

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est6:\*

15: em\_estom:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444.8	98.0	2765	11 AK052947	AK052947 Mus muscu
2	1444.8	98.0	3244	11 AK033734	AK033734 Mus muscu
3	1444.8	98.0	3405	11 AK042767	AK042767 Mus muscu
4	1366.2	92.7	2893	11 BC029099	BC029099 Mus muscu

5	873.6	59.3	902	13	BUS17879	BUS17879
6	865.4	58.7	2502	11	AK081347	AK081347 Mus muscu
7	840	57.0	2826	11	BC041783	BC041783 Homo sapi
8	809	54.9	823	13	BU614825	UI-M-EV0-
9	757.6	51.4	2655	11	BC051876	BC051876 Homo sapi
10	707	48.0	901	13	BQ957838	BQ957838 AGENCOURT
11	616.4	41.8	999	13	BQ068266	BQ068266 AGENCOURT
12	597.6	40.5	910	10	BG243001	BG243001 602355974
13	595.6	40.4	877	10	BF137533	BF137533 601780532
14	595	40.4	712	12	BI693338	BI693338 603343666
15	562.2	38.1	677	10	BB662450	BB662450 BB662450
16	559	37.9	559	12	BM053896	BM053896 idg9c11.y
17	551.8	37.4	584	10	BF151395	BF151395 uz15b12.y
18	534.2	36.2	994	13	BUS54214	BUS54214 AGENCOURT
19	531	36.0	811	10	BG185961	BG185961 RST4916 A
20	519.8	35.3	523	10	BF021679	BF021679 uy50f05.y
21	511	34.7	511	9	AW210331	AW210331 ul53f09.y
22	497.2	33.7	721	13	BQ443526	BQ443526 UI-M-EW0-
23	456.2	30.9	609	10	BF133918	BF133918 601779154
24	448.4	30.4	695	12	BI668022	BI668022 603295848
25	446.6	30.3	478	12	BM022835	BM022835 1462e12.y
26	445.4	30.2	447	10	BF011835	BF011835 ua37d10.y
27	441.2	29.9	902	10	BF163629	BF163629 601769732
28	440.2	29.9	770	12	BI556877	BI556877 603239918
29	439	29.8	789	12	BI911795	BI911795 603065222
30	434.2	29.5	982	13	BU459467	BU459467 603368015
31	432.6	29.3	567	12	BM827309	BM827309 K-EST0099
32	415.4	28.2	1029	10	BG173847	BG173847 602333906
33	413.6	28.1	676	13	BU259419	BU259419 603415593
34	406.6	27.6	562	9	AU280428	AU280428 AU280428
35	405	27.5	521	10	BE374398	BE374398 601227568
36	404.4	27.4	408	10	BE304156	BE304156 601085830
37	400	27.1	400	9	AL364180	AL364180 AL364180
38	392.8	26.6	864	10	BF137524	BF137524 601780523
39	389.4	26.4	423	14	CB797465	CB797465 AMGNNUC:S
40	388.8	26.4	1142	10	BG681390	BG681390 602627750
41	382.2	25.9	411	14	CB802513	CB802513 AMGNNUC:S
42	379.6	25.8	980	13	BU527807	BU527807 AGENCOURT
43	374.2	25.4	399	13	BY018563	BY018563 BY018563
44	371.6	25.2	556	10	BG609411	BG609411 323251 MA
45	357.4	24.2	769	14	CB309471	CB309471 AGENCOURT

#### ALIGNMENTS

RESULT 1	AK052947	2765 bp	linear	HTC 05-DEC-2002
LOCUS	AK052947	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930001M08 product:platelet-derived growth factor, C polypeptide, full insert sequence.		
DEFINITION	AK052947			
ACCESSION	AK052947.1	GI:26343118		
VERSION	AK052947.1			
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			

REFERENCE AUTHORS	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Oneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Koyada, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE		RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL MEDLINE PUBMED		Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE AUTHORS	4	20530913 11076861 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Sato, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, I., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Hoffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
TITLE		Functional annotation of a full-length mouse cDNA collection
JOURNAL MEDLINE PUBMED		Nature 409 (6821), 685-690 (2001)
REFERENCE AUTHORS	5	21085660 11217851 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL MEDLINE PUBMED		Nature 420, 563-573 (2002)
REFERENCE AUTHORS	6	(bases 1 to 2765) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE		Direct Submission
JOURNAL		Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers
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RESULT 2  
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LOCUS  
DEFINITION  
Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403008 product:platelet-derived growth factor, C polypeptide, full insert sequence.  
AK033734  
ACCESSION  
VERSION  
KEYWORDS  
AK033734 3244 bp mRNA linear HTC 05-DEC-2002  
HTC; CAP trapper.

SOURCE ORGANISM	Mus musculus (house mouse)
REFERENCE AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Chata, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Maeda, H., Ashburner, M., Batalov, S., Casavant, P., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staudli, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Anon, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, J., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombarts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	6 (bases 1 to 3244)
PUBMED	1217851
REFERENCE AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

TITLE  
 JOURNAL  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/  
 Location/Qualifiers  
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QY	1442	ACCAAGAGGAGTCATCAAGACACTGC	1470
Db	1997	ACCAAGAGGAGTCATCAAGACACTGC	2025
RESULT 3			
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LOCUS			
DEFINITION	AK042767	3405 bp mRNA linear	HTC 05-DSC-2002
		Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length	
		enriched library, clone:A730022G11 product:platelet-derived growth	
		factor, C polypeptide, full insert sequence.	
ACCESSION	AK042767		
VERSION	AK042767.1	GI:26335314	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	20493374		
MEDLINE	11042159		
PUBMED			
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
	Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,		
	Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
	Fujwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,		
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
	RIKEN integrated sequence analysis (RISA) system--384-format		
	sequencing pipeline with 384 multipillar sequencer		
	Genome Res. 10 (11), 1757-1771 (2000)		
JOURNAL	20530913		
MEDLINE	11076861		
PUBMED			
REFERENCE			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,		
	Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,		
	Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,		
	Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,		
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	Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,		
	Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,		
	Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,		
	Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,		
	Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,		
	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,		
	Toyo-oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,		
	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.		
	and Hayashizaki, Y.		
	Functional annotation of a full-length mouse cDNA collection		
	Nature 409 (6821), 685-690 (2001)		
JOURNAL	21085660		
MEDLINE			

11217851			
5			
REFERENCE			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research		
	Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
	of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 3405)		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,		
	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,		
	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,		
	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,		
	Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,		
	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,		
	Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,		
	Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,		
	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,		
	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,		
	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,		
	Muramatsu, M. and Hayashizaki, Y.		
	Direct Submission		
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of		
JOURNAL	Physical and Chemical Research (RIKEN), Laboratory for Genome		
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),		
	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,		
	Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,		
	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,		
	Fax:81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome		
	Encyclopedia Project of Genome Exploration Research Group in Riken		
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.		
	Division of Experimental Animal Research in Riken contributed to		
	prepare mouse tissues.		
	Please visit our web site for further details.		
	URL:http://genome.gsc.riken.go.jp/		
	URL:http://fantom.gsc.riken.go.jp/.		
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	SIIMPOVTTTSPVLPSSLSLDLNNAVTAFSTLEELIRLYEPDWDLDLYKP		
	TWQLLKAPLYGKSKVNLKKEVKLYSCTPRNFSVIRELKTDFIWFPGCLL		
	VKRCGNACCLGKNECCQVPRVTKTKTHEVLQRPKTVGKGLSLTDVALEHHE		
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT      224 a      233 c      240 g      205 t
ORIGIN
Query Match      59.3%; Score 873.6; DB 13; Length 902;
Best Local Similarity 99.3%; Pred. No. 3e-234;
Matches 896; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 54 GGAACCTACCTCGATTCCTCTGCTGCGAGCGCGCGGCTTCCACGCGAGCGAG 113
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QY 114 CTTTCCCGGGCTGGGCTTGAGCTTGGAGTCGTGCTTCCCGAGTGCCTCCCGGAGTG 173
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QY 174 AGCCCTCGCCCGAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCT 233
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QY 234 GGCCGGCAAGAAACGGGAGCTCGGGCTGAGTCAACTGAGCGAGCAAGTTGCGAGCTC 293
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QY 534 GCCCAGTGATGGAAGTGTTTTGGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAAGCA 593
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RESULT 6
AK081347
LOCUS
DEFINITION
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:CL30008P20 product:platelet-derived growth factor,
C polypeptide, full insert sequence.
ACCESSION
AK081347.1 GI:26099857
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsumi,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,K.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsui,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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Wyshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
```



REMARK  
COMMENT

USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mdpaxil.stanford.edu](mailto:mdpaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 4i Row: q Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186  
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RESULT 8  
BU614825

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DEFINITION  
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UI-M-EV0-cbh-b-02-0-UI 5', mRNA sequence.

ACCESSION  
BU614825

VERSION  
BU614825.1

KEYWORDS  
EST.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 823)

AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
Unpublished

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

Tissue Procurement: Dr. James Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5

Location/Qualifiers

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a	201 c	196 q	204 t	3 others

BASE COUNT  
ORIGIN

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Query Match  
Best Local Similarity 34.5%; SCORE 809; DB 13; Length 823;  
Best Local Similarity 99.5%; Pred. No. 4.3e-216;

BEST LOCAL SIMILARITY 99.5%; Pred: NO. 4.3e-216;  
Matches 820: Conservative 0: Mismatches 3: Indels 1: Gaps 1:

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QY 1005 CTGGCCAGTTGTCTCCTGGTCAAGCGCTGTGGAGGAAATTGTGCTCTCCATAA 1064

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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [md@paxil.stanford.edu](mailto:md@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 110 Row: p Column: 4  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186  
This clone has the following problem: frame shifted.

## FEATURES

source

1. 2655  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6527736"  
/tissue\_type="Uterus, leiomyosarcoma"  
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/lab\_host="DH10B"  
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BASE COUNT 822 a 479 c 551 g 803 t

## ORIGIN

Query Match 51.4%; Score 757.6; DB 11; Length 2655;  
Best Local Similarity 79.6%; Pred. No. 2.6e-201;  
Matches 936; Conservative 0; Mismatches 179; Indels 61; Gaps 1;  
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16 GGAGTCGTGCTCCAAAGTCCCGCGCGTGGAGTGGAGTCTCCAGCCAGTCCAGCAATGA 75  
200 TCCTCTCGGCTCTCTGTGATCATCTGCTGCGCGCGCGCAAGACGGGCTCGGG 259  
76 GCCTCTTCGGGCTCTCTGCTGATCATCTGCTGCGCGCGCGCGAGAGCGGGACTCAGG 135  
260 CTGAGTCCAACTGAGCAGCAAGTTGCAAGTCTCCAGCGCAAGCAAGCAAGCAAC----- 312  
136 CGGAATCCAACTGAGTAGTAATTTCCAGTCTTCCAGCAACAGCAAGCAAGCAAGTAGGA 195  
313 -----GGAGTG 318  
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319 CAAGATCCCGCGATGAGAGAGTGTCACTATATCTGTAATGGAGCATCCAGACCGG 378  
256 CAAGATCCCGATGAGAGATTAATTAAGTGTGCTACTAATGGAAGTATTCAGGCCCA 315  
379 AAGTTTCCTCATAGTACCCCAAGAAATATGGTGTGGTGTGGAGATTAGTTGCAGTAGAT 438  
316 AGGTTTCCTCATAGTATCCCAAGAAATACGGTCTTGGTATGGAGATTAGTACGATAGAG 375  
439 GAAATGTGCGATCCAGTCCAGTCCATTTGATGAGAGATTGGCTGGAGATCCAGAAAGC 498  
376 GAAATGTGATGATACACATTAACGTTTATGAAGATTGGCTTGAAGACCCAGAAAGAT 435  
499 GATATATCAAGTATGATTTTGTAGAAGTGGAGAGCCAGTGTAGTGAAGTGTTTTAGGA 558  
436 GACATATGCAAGTATGATTTTGTAGAAGTGGAGACCCAGTGTAGGAACTATATTAGGG 495  
559 CGCTGGTGTGTTCTGGAGCTGTGCCAGAAAGCAGACTTCTAAAGGAAATCATATCAGG 618  
496 CGCTGGTGTGTTCTGGTACTGTATCCAGGAAACAGATTCTTAAAGGAAATCAAAATTAGG 555  
619 ATAGATTTGATCTGATGAGTATTTTCCATCTGAACCGGATTTCTGCATCCACTACAGT 678  
556 ATAGATTTGATCTGATGAGTATTTTCCATCTGAACCGGATTTCTGCATCCACTACAGT 615  
679 ATTATCATGCCAAGTCCAGAAACACCGAGTCTCTCGGTGTTCGCCCTTCTCATCTTTG 738  
616 ATTGATGCCCAAAATTCAGAGAGCTGTGAGTCTCTTCAAGTCTACCCCTTCAGCTTTG 675

Qy 739 TCATTGGACCTGCTCAAAATGCTGTCACTGCCCTTCACTACCTTTGGAGAGCTGATTGG 798  
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Qy 799 TACCTAGAGCAGATCGATGGCAGGTGAGTGGACAGCCTCTACAGCCCAACATGGCAG 858  
Db 736 TATCTTGAACAGAGATGGCAGTGGACCTTAGAAGATCTATAGGCCCACTTGGCAA 795  
Qy 859 CTTTGGGCAAGCTTCTCTGTATGGGAAAAAGCAAGTGGTGAATCTCAATCTCTCCTC 918  
Db 796 CTTTGGGCAAGCTTCTCTGTATGGGAAAAAGCAAGTGGTGAATCTCAATCTCTCCTC 855  
Qy 919 AAGGAAGAGGTAAACCTCTACAGTGCACACCCCGGAACCTTCTCAGTGTCCATACGGGAA 978  
Db 856 ACAGAGGAGGTAAAGATTATACAGCTGCACACCTGTAACCTCTCAGTGTCCATAGGAA 915  
Qy 979 GAGCTAAAGAGGACAGATACCATATCTGCGCAGGTGTCTCCTGCTCAAGCGCTGTGA 1038  
Db 916 GAACCTAAAGAGACCGGATACCATATCTGCGCAGGTGTCTCCTGCTCAAGCGCTGTGT 975  
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Qy 1099 AAAAAAAGTACCATGAGTCTCTTCACTGTGAGACCAAAAACTGGAGTCAAGGATTTGCAT 1158  
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Qy 1219 AAGCAGAGGAGTAACTGACGCTTCTGAGCAGCAAC 1254  
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BO957838 901 bp mRNA linear EST 21-AUG-2002  
AGENCOURT 8860959 NCI CGAP\_Mam2 Mus musculus cDNA clone  
IMAGE:6440547 5', mRNA sequence.  
BO957838  
EST.  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgi.nci.nih.gov/>.  
1 (bases 1 to 901)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [csapbs-remail.nih.gov](mailto:csapbs-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L1AM13962 row: f column: 04  
High quality sequence stop: 669.  
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FEATURES  
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 257 a 212 c 225 g 206 t 1 others
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Best Local Similarity 99.7%; Pred. No. 2.3e-187; Indels 0; Gaps 0;
Matches 707; Conservative 0; Mismatches 2;

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Qy 822 GTTGGACTTGACAGCTCTACAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTGA 881
Db 61 GTTGGACTTGACAGCTCTACAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTGA 120

Qy 882 TGGGAAAAAAGCAAGTGGTGAATCTCTCAAGGAGAGGTAAACCTCTACAG 941
Db 121 TGGGAAAAAAGCAAGTGGTGAATCTCTCAAGGAGAGGTAAACCTCTACAG 180

Qy 942 CTGCACACCCCGGAATCTTCAGTGTCCATACGGGAAGAGCTAAAGAGCAGATACCAT 1001
Db 181 CTGCACACCCCGGAATCTTCAGTGTCCATACGGGAAGAGCTAAAGAGCAGATACCAT 240

Qy 1002 ATTCTGCCAGGTGTCTCTGCTGTCAGCCGCTGGGAGGAATGTGCTGTGTCTCCA 1061
Db 241 ATTCTGCCAGGTGTCTCTGCTGTCAGCCGCTGGGAGGAATGTGCTGTGTCTCCA 300

Qy 1062 TAATTGCAATGAATGTGAGTGTGTCACCGTAAAGTTTACAAAAAGTACCATGAGTCTCT 1121
Db 301 TAATTGCAATGAATGTGAGTGTGTCACCGTAAAGTTTACAAAAAGTACCATGAGTCTCT 360

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Db 361 TCAGTTGAGACCAAAACTGGAGTCAAGGAGTTCATAGTCACTGATGCGCTCT 420

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Db 481 TTGCTAGCAGCACACGTGAGCACTTGTGTATCTGTGTACCCCAAGCAACTTTCATCCC 540

Qy 1302 CACAGCGTTGGCGCAGGCTCTCAGCTGTGATGTGCTGTATGTTAAAGATCTTACTC 1361
Db 541 CACAGCGTTGGCGCAGGCTCTCAGCTGTGATGTGCTGTATGTTAAAGATCTTACTC 600

Qy 1362 GTCTCCAAACCAATCTCAGTGTGTTTCTTCAATAGCTTCCCTCGCAGGACTTCAAGTG 1421
Db 601 GTCTCCAAACCAATCTCAGTGTGTTTCTTCAATAGCTTCCCTCGCAGGACTTCAAGTG 660

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RESULT 11
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LOCUS
DEFINITION AGENCOURT_6794408 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770510
5', mRNA sequence.
ACCESSION BQ068266
VERSION BQ068266.1 GI:19897312
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 999)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12833 row: k column: 23
High quality sequence stop: 676.
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Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH MGC Library."
BASE COUNT 290 a 213 c 235 g 261 t
ORIGIN
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Query Match 41.8%; Score 616.4; DB 13; Length 999;
Best Local Similarity 83.1%; Pred. No. 7.8e-162;
Matches 738; Conservative 0; Mismatches 146; Indels 4; Gaps 3;

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Qy 288 GCTCTCCAGCAGCAAGGAACAGACGAGTCGAGATCCCGCATGAGAGTTGTCAC 347
Db 61 GTTTTCAGGCAACAGGAACAGACGAGTACAGATCCTCAGCATGAGAAATTTATAC 120

Qy 348 TATATCTGTAATGGGAGCATCCACAGCCGGAAGTTTCTCATACGTACCCAGAAATAT 407
Db 121 TGTTCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTATTCAGAAATAC 180

Qy 408 GGTGCTGCTGTGAGATAGTTGTCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGA 467
Db 181 GGTCTTGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATACAACTTACGTTGA 240

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Db 301 TGAGGAGCCCAAGTATGGAAGTATATATAGGCGCTGGTGTGTTCTGGTACTGTACCAGG 360

Qy 588 AAGCAGACTTCTAAAGGAAATCATATCAGATAAGATTTGTATCTGATGAGTATTTTCC 647
Db 361 AAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATTTTCC 420

Qy 648 ATCTGAACCGGATTTCTGCATCCACTACATATATCATGCCACAGTCTCAGAGAACAC 707
Db 421 TTCTGAACCGGTTTCTGCATCCACTACATATTTGTTCATGCCACATTTCAAGAAGCTGT 480
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QY 708 GAGTCCTCGGTGTTGCCCTTTCATCTTGTGTCATGGACCTGCTCAACAATGCTGTGAC 767
Db 481 GAGTCCTTCAGTGTCTACCCCTTCAGCTTTGCCACCTGACCTGCTTAATAATGCTATAAC 540

QY 768 TGCCCTTCAGTACCTTGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGA 827
Db 541 TGCCCTTAGTACCTTGAAGACCTTATCGATATCTTTGAACACAGAGATGGCAGTTGGA 600

QY 828 CTTGGACAGCCTCTACAGCAACATGGAGCTTTTGGGCAAGCTTTCTGTCATGGAA 887
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QY 888 ABAAGCAGAGTGTGAATCTGAATCTCCTCAAGAGAGAGTAAACTCTACAGCTGCAC 947
Db 661 ABAATCCAGAGTGTGAATCTGAATCTCTAAACAGAGAGTAAAGTATATACAGCTGCAC 720

QY 948 ACCCCGGAATCTTCAGTGTCC--ATACGGGAAGAGCTAAAGAGGAGCAGATACCA-TATT 1004
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QY 1005 CTGGCCAGGTGTCTCTGTCAGGCTGTGGAGGAATGTGCTGTTGTCCTCCATAA 1064
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QY 1065 TTGCAATGAATGT-CAGTGTGTCCTCAGCTAAAGTTACAAAAAAGTACC 1111
Db 841 TTGCAATGAATGTCCATGGTGTCCCAAGCAAGTTCTCAAAAAATAAC 888

RESULT 12
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LOCUS 60235974F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',
DEFINITION mRNA sequence.
ACCESSION BG243001
VERSION BG243001.1 GI:12752725
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 910)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 242 a 220 c 250 g 198 t

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## ORIGIN

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Query Match 40.5%; Score 597.6; DB 10; Length 910;
Best Local Similarity 95.4%; Pred. No. 1.4e-156;
Matches 701; Conservative 0; Mismatches 25; Indels 9; Gaps 8;

QY 736 TTGTCAATGGACCTGCTCAACAATGCTGTGACCTGTCCTTCAAGTACCTTTGGAAGAGCTGATT 795
Db 22 TTGTCAATGGACCTGCTCAACAATGCTGTGACCTTCAAGTACCTTTGGAAGAGCTGATT 80

QY 796 CGGTACTTAGAGCCAGATCGATGCGAGGTGACCTTGGACAGCCTCTACAGCCACACATGG 855
Db 81 CGGTACTTAGAGCCAGATCGATGCGAGGTGACCTTGGACAGCCTCTACAGCCACACATGG 140

QY 856 CAGCTTTTGGGCAAGCTTTCTCTGTATGGAAAAAGAAAGTGGTGAATCTTGAATCTC 915
Db 141 CAGC-TTTGGGCAAGCTTTCTCTGTATGGAAAAAGAAAGTGGTGAATCTTGAATCTC 199

QY 916 CTCAAGGAAGAGGTAAACCTCTACAGCTGCACACCCCGGAACCTTTCAGTGTCCATACGG 975
Db 200 CTCAAGGAAGAGGTAAACCTCTACAGCTGCACACCCCGGAACCTTTCAGTGTCCATACGG 259

QY 976 GAAGACTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTCTGCTCAAGCGCTGT 1035
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QY 1036 GGAGGAAATGTGCTGTTCTCCATAATTTGCAATGAATGTAGTGTGTCCTCCACGTAAA 1095
Db 320 GGAGGAAA-TGTGCTGTTGTCTCCATAATTTGCAATGAATGTAGTGTGTCCTCCACGTAAA 378

QY 1096 GTTACAAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAAACTGGAGTCAAGGGATTG 1155
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QY 1156 CATAAGTCACTCACTGATGTGGCTCTGGAACACACAGCAAGTGTGCTGTGTGTGAGA 1215
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QY 1216 GGAACGCGAGGAGGTAACTGCGAGCCTTCTAGCAGCACACGTGAGCA-CTGGCATTTCTG 1274
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QY 1275 TGTACCCCCCAACAGCAACCTTTCATCCCAACAGCGTTGGCGGAGGCTCTCAGCTGCTG 1334
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QY 1335 ATGCTGCTATGTAAAGATCTTACTGCTTCCACCAAAATTTCTCAGTTGTTGCTTCAA 1394
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QY 1395 TAGCCTTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAAAGACAGAGGACCAANAGGAGTC 1454
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QY 1455 AATCACAAGACACTG 1469
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LOCUS 601780532F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008799 5',
DEFINITION mRNA sequence.
ACCESSION BF137533
VERSION BF137533.1 GI:10976573
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

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TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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Location/Qualifiers

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Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 221 a 220 c 233 g 203 t

ORIGIN

Query Match 40.4%; Score 595.6; DB 10; Length 877;  
Best Local Similarity 91.3%; Pred. No. 5.2e-156;  
Matches 665; Conservative 0; Mismatches 59; Indels 4; Gaps 3;

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QY 374 GCCCGAAGTTTCTCTACATCCCAAGAAATATGGTGGTGGAGATGAGTGCAG 433  
DB 90 GCCCGAAGTTTCTCTACATCCCAAGAAATATGGTGGTGGAGATGAGTGCAG 149  
QY 434 TAGATGAAATATGCGGATCCAGTGCATTTGATGAGAGATTTGGCTCGAAGATCCAG 493  
DB 150 TAGATGAAATATGCGGATCCAGTGCATTTGATGAGAGATTTGGCTCGAAGATCCAG 209  
QY 494 AAGACGATATATCAAGTATGATTTGTAGAGTTGAGGAGCCAGTGGAGTGT 553  
DB 210 AAGACGATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTGGAGTGT 269  
QY 554 TAGGACGCTGGTGTGGTCTGCGGAGCTGCGCAGGAAAGCAGACTTCTAAGGAAATCAT 613  
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DB 330 TCAGGATAGATTTGATCTGATGAGTATTTTCATCTGACCCGAGATTTGATCTCACT 389  
QY 674 ACAGTATATCATGCCACAGTACAGAAACCCAGGCTCTCGGTCTGCCCTTCAT 733  
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DB 450 CTTTGTCTATGGACCTCTCAACAAATCTGTGACTGCTTCAGTACCTTGG-AAGAGCTG 509  
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Db 570 TGGCAGCTTTCTGGGCAAGGTTTCCTGTATGGGAACACACAGCAAGGTGAATCTGAAT 629  
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QY 971 TAGCGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCTCTGCTCAAGC 1030  
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Db 749 GGGGACGA 756

RESULT 14  
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603343666F1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5371337 5',  
mRNA sequence.  
ACCESSION BI693338  
VERSION BI693338.1 GI:15655967  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 712)  
NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11945 row: c column: 18  
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BASE COUNT 205 a 174 c 171 g 162 t

ORIGIN

Query Match 40.4%; Score 595; DB 12; Length 712;  
Best Local Similarity 99.7%; Pred. No. 6.7e-156;  
Matches 606; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 864 GGCGAAGGCTTTCTGTATGGGAAAAAGCAAGTGGTGAATCTGAATCTCTCAAGGA 923  
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QY 924 AGAGGTAAAACTCTACAGCTGCACACCCCGAACTTCTCAGTGTCCATAGCGGAGAGCT 983  
Db 61 AGAGGTAAAACTCTACAGCTGCACACCCCGAACTTCTCAGTGTCCATAGCGGAGAGCT 120  
QY 984 AAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCTCTGGTCAAGCGCTGTGGAGAAA 1043



Db 317 AAAGAACGGGGAAGCTCGGGCTGAGTCCAAACCTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 376  
QY 302 AGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 361  
Db 377 AGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 436  
QY 362 GGAGCATCCACAGCCCGGAAGTTTCCTCATACGTACCCCAAGAAATATGGTCTGGTGTGGA 421  
Db 437 GGAGCATCCACAGCCCGGAAGTTTCCTCATACGTACCCCAAGAAATATGGTCTGGTGTGGA 496  
QY 422 GATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGCATTTGATGAGAGATTGGGC 481  
Db 497 GATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGCATTTGATGAGAGATTGGGC 556  
QY 482 TGGAAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCCAAGTG 541  
Db 557 TGGAAAGATCCAGAGACGATATATGNCAGTATGATTTTGTAGAAAGTTGAGAGCCCAAGTG 616  
QY 542 ATGGAAGTGTTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 601  
Db 617 ATGGAAGTGTTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGG-AAACAGACTTCTA 675  
QY 602 A 602  
Db 676 A 676

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Job time : 2158.47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:13 ; Search time 35.9375 Seconds  
(without alignments)  
1523.775 Million cell updates/sec

Title: US-09-852-209a-7

Perfect score: 1848

Sequence: 1 MLLGLLLTSLAAGRTGT.....DVALEHHEBCDCVCRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	21	Mouse zveg3, SEQ
2	1848	100.0	345	21	Murine vascular en
3	1848	100.0	345	21	A murine platelet-
4	1848	100.0	345	22	Mouse zveg3 prote
5	1848	100.0	345	23	Mouse VEGF-like pr
6	1848	100.0	345	23	Mouse zveg3. Mus
7	1848	100.0	345	23	Mouse platelet-der
8	1848	100.0	345	24	Mouse growth facto
9	1667	90.2	345	20	Human VEGF-E prote

10	1667	90.2	345	20	AAV41766	Human PRO200 prote
11	1667	90.2	345	20	AAV30023	Human vascular end
12	1667	90.2	345	21	AAV48657	Human zveg3, SEQ
13	1667	90.2	345	21	AAV42450	Human platelet-der
14	1667	90.2	345	21	AAV44322	Human PRO200 (UNQ1
15	1667	90.2	345	21	AAV10633	Human RACE generat
16	1667	90.2	345	21	AAV10635	Human VEGF-X prote
17	1667	90.2	345	21	AAV10644	Human VEGF-X prote
18	1667	90.2	345	21	AAV10650	Human 990126vegk p
19	1667	90.2	345	21	AAV10651	Human VEGF-X prote
20	1667	90.2	345	21	AAV19578	Human PRO200 (vasc
21	1667	90.2	345	21	AAV33414	Human PRO200 prote
22	1667	90.2	345	21	AAV24412	Human PRO713 prote
23	1667	90.2	345	21	AAV01419	Human TANGO 128.
24	1667	90.2	345	21	AAV96858	Human growth facto
25	1667	90.2	345	21	AAV59285	Bone morphogenic p
26	1667	90.2	345	22	AAV65603	Human zveg3 polyp
27	1667	90.2	345	22	AAU08465	Polypeptide for hu
28	1667	90.2	345	22	AAU12314	Human PRO200 polyp
29	1667	90.2	345	22	AAV74028	Human VEGF/PDGF-11
30	1667	90.2	345	22	AAE02649	Human LP8, a PDGF-
31	1667	90.2	345	22	AAE00997	Human zveg3 prote
32	1667	90.2	345	22	AAV50980	Human PRO200 prote
33	1667	90.2	345	22	AAV49895	Human angiogenesis
34	1667	90.2	345	22	AAV53074	Human vascular end
35	1667	90.2	345	23	ABV79984	Human VEGF-like pr
36	1667	90.2	345	23	ABG92889	Human VEGF/PDGF-11
37	1667	90.2	345	23	ABB81331	Human zveg3. Hom
38	1667	90.2	345	23	AAV47889	Human zveg3 prote
39	1667	90.2	345	23	AAU76884	Human growth facto
40	1667	90.2	345	24	ABG76393	Human PRO polypept
41	1667	90.2	345	24	ABU66712	Human secreted/tra
42	1667	90.2	345	24	ABU66988	Novel secreted and
43	1667	90.2	345	24	ABU59793	Human PRO200 polyp
44	1667	90.2	345	24	ABU61152	Human vascular end
45	1667	90.2	345	24	ABG72132	

#### ALIGNMENTS

##### RESULT 1

AAV48658  
ID AAV48658 standard; Protein; 345 AA.

XX AAV48658;

XX AC

XX 09-MAR-2001 (first entry)

XX Mouse zveg3, SEQ ID NO:35.

XX Mouse; zveg3; zveg4 fusion; growth factor homologue; VEGF/PDGF family;

XX murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;

XX neovascularisation; tissue repair; proliferation; differentiation;

XX liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;

XX periodontal disease; bone fracture; wound healing; vulnery; ischaemia;

XX immunomodulation; hepatic.

XX Mus musculus.

XX WO200066736-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000WO-US40047.

XX 03-MAY-1999; 99US-0304216.

XX 10-NOV-1999; 99US-0164463.

XX 04-FEB-2000; 2000US-0180169.

XX (ZYMO ) ZYMOGENETICS INC.

XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI; 2000-687541/67.  
DR N-PSDB; AAC81583.  
XX  
PT Growth factor homologs and the nucleic acids that encode them, useful  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease -  
XX  
PS Disclosure; Page 130-131; 143pp; English.  
XX  
CC The invention relates to the human growth factor homologue zvegfg4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)  
CC characterised by a PDGF cysteine knot structure, and a CUB domain  
CC (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like  
CC activity, having mitogenic activity on fibroblasts, vascular smooth  
CC muscle cells and pericytes, and has also been shown to stimulate bone  
CC growth. The invention also relates to fusion proteins comprising human  
CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3  
CC fusions; expression constructs and host cells comprising human zvegfg4  
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody  
CC which binds to human zvegfg4 or a fragment thereof; a method of activating  
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a  
CC method of modulating the proliferation, differentiation, migration or  
CC metabolism of bone cells, comprising exposing bone cells to  
CC zvegfg4-derived polypeptides; and a method of detecting a genetic  
CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived  
CC fragments may be used to stimulate tissue development or repair, or  
CC cellular differentiation or proliferation. They are particularly used for  
CC the treatment or repair of liver damage, and may also be used to  
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
CC multiple sclerosis). Due to their osteogenic activity, they may also be  
CC in the treatment of periodontal disease and fractures. They may also be  
CC used to enhance expansion and mobilisation of haematopoietic stem cells  
CC and endothelial precursor stem cells, which may be useful in the  
CC treatment of ischaemia, in wound healing, and in the modulation of the  
CC immune system. The present sequence represents mouse zvegfg3.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLLGLLLLSALAGQGTGRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
QY 61 PKFHTYPRNNVLVRLVAVDENVRILQTFDERFGLDPEDDICKYDFVEVEPDSGSLV 120  
DB 61 PKFHTYPRNNVLVRLVAVDENVRILQTFDERFGLDPEDDICKYDFVEVEPDSGSLV 120  
QY 121 GRWCGSGTVPKQTSKGNHRIKRVSDYEPSEFGCIHYSIIMPQVTTSPSVLPSS 180  
DB 121 GRWCGSGTVPKQTSKGNHRIKRVSDYEPSEFGCIHYSIIMPQVTTSPSVLPSS 180  
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RESULT 2  
RAY96861  
ID AAY96861 standard; Protein; 345 AA.

XX AAY96861;  
XX 26-SEP-2000 (first entry)  
DT Murine vascular endothelial growth factor homologue, ZVEGF3.  
DB  
XX Vascular endothelial growth factor; homologue; zvegfg3; CUB domain;  
XX Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;  
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;  
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;  
KW vulnery.  
XX Mus musculus.  
OS WO200034474-A2.  
XX  
XX 15-JUN-2000.  
XX 07-DEC-1999; 99WO-US28968.  
XX 07-DEC-1998; 98US-0207120.  
XX 06-JUL-1999; 99US-0142576.  
XX 21-OCT-1999; 99US-0161653.  
XX 12-NOV-1999; 99US-0165255.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
PI Gilbertson DG, West JW;  
XX WPI; 2000-4234420/36.  
XX N-PSDB; AAA51527.  
XX Novel zvegfg3 polypeptides and nucleotides encoding them useful for  
XX stimulating growth of smooth muscle cells and fibroblasts comprising an  
XX epitope bearing portion of a specific amino acid sequence  
XX Claim 1; Page 169-170; 173pp; English.  
XX  
XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor  
XX homologue. Polypeptides comprising an epitope-bearing portion human or  
XX murine ZVEGF3 are claimed. The growth factors comprise a growth factor  
XX domain and a CUB domain (generic sequence motifs are shown in AAY96859  
XX and AAY96860). The growth factor domain is characterized by an  
XX arrangement of cysteine residues and beta-strands that is characteristic  
XX of the "cysteine knot" structure of the platelet-derived growth factor  
XX (PDGF) family. The CUB domain shows homology to CUB domains in  
XX neuropilins, human bone morphogenetic protein-1, porcine seminal plasma  
XX protein, bovine acidic seminal fluid protein and Xenopus laevis  
XX tolloid-like protein. Structural analysis and homology predict that  
XX ZVEGF3 polypeptides complex with a second polypeptide to form multimeric  
XX proteins. The human zvegfg3 gene has been mapped to chromosome 4q28.3.  
XX ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth  
XX muscle cells, for activating cell surface PDGF-alpha receptor and for  
XX inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is  
XX useful for regulating (post-development) organ growth, regeneration and  
XX maintenance, as well as tissue maintenance and repair processes. ZVEGF3  
XX antagonists are useful for treating cancer, rheumatoid arthritis,  
XX diabetic retinopathy, ischemic limb disease, peripheral vascular  
XX disease, myocardial ischemia, vascular intimal hyperplasia,  
XX atherosclerosis, wound healing, chronic liver disease and haemangioma  
XX formation. ZVEGF3 can also be used to modulate neurite growth and  
XX development of the nervous system, and for treating neurodegenerative  
XX diseases.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGQGTGRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60





PN WO200128586-A1.  
XX  
XX  
XX 26-APR-2001.  
XX  
XX 23-OCT-2000; 2000WO-US29270.  
XX  
XX 21-OCT-1999; 99US-0161653.  
PR 12-NOV-1999; 99US-0165255.  
PR 01-AUG-2000; 2000US-0222223.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gilbertson DG;  
XX  
XX WPI; 2001-300278/31.  
DR N-PSDB; AAD04650.  
XX  
XX Use of zvegf3 antagonist for reducing fibroproliferative disorder of  
PT kidney, liver and bone, reducing extracellular matrix production,  
PT treating fibrosis or reducing stellate cell activation in mammal -  
XX  
XX Example 2; Fig 2; 70pp; English.  
XX  
XX The patent discloses materials and methods for reducing cell  
CC proliferation or extracellular matrix production, treating fibrosis and  
CC reducing stellate cell activation in a mammal. The method comprises  
CC administering a composition containing a zvegf3 antagonist in combination  
CC with a delivery vehicle. The zvegf3 is a protein that is structurally  
CC related to platelet-derived growth factor (PDGF) and the vascular  
CC endothelial growth factors (VEGF). The zvegf3 protein is also designated  
CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the  
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat  
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active  
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and  
CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as  
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic  
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders  
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,  
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,  
CC fibrotic disorders of pancreas, fibroproliferative disorders of the  
CC vasculature such as transplant vasculopathy and fibroproliferative  
CC disorders of the bone such as osteopetrosis and hyperostosis.  
CC The present sequence is mouse zvegf3 protein.  
XX  
SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 22; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISNGSISHS 60  
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISNGSISHS 60  
Qy 61 PKFHTYPRNNVLVWRLVAVDENVRILQTFDERFGLDEPDIDCKYDFVEEESDGSVL 120  
Db 61 PKFHTYPRNNVLVWRLVAVDENVRILQTFDERFGLDEPDIDCKYDFVEEESDGSVL 120  
Qy 121 GRWCGSVTPGKQTSKGNHRIKRVSDYFVPEPGFCFHYSLIMPQVTTTSPSLPPSS 180  
Db 121 GRWCGSVTPGKQTSKGNHRIKRVSDYFVPEPGFCFHYSLIMPQVTTTSPSLPPSS 180  
Qy 181 LSLDLLNNAVTAFTSLLEILRYLEPRDQVLDLSLYKFTWQLGKAFYLGKSKVNNLNL 240  
Db 181 LSLDLLNNAVTAFTSLLEILRYLEPRDQVLDLSLYKFTWQLGKAFYLGKSKVNNLNL 240  
Qy 241 LKEEVLYSCFPRNPSVIRELKRDTDFWPGCLLVRCGNCACCLHNCNECQVPRK 300  
Db 241 LKEEVLYSCFPRNPSVIRELKRDTDFWPGCLLVRCGNCACCLHNCNECQVPRK 300  
Qy 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5  
ABG92894  
ID ABG92894 standard; Protein; 345 AA.  
XX  
XX AC ABG92894;  
XX  
XX DT 19-NOV-2002 (first entry)  
XX  
XX DE Mouse VEGF-like protein zvegf 3.  
XX  
XX VEGF; vascular endothelial growth factor; zvegf 3; mouse;  
KW chromosome 3; cell proliferation; differentiation; metabolism;  
KW migration; revascularisation; solid tumour; diabetic retinopathy;  
KW psoriasis; rheumatoid arthritis; cancer; autoimmune disease;  
KW inflammation; myocardial ischaemia; scleroderma; fibrosis;  
KW glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;  
KW skin grafting; female reproductive tract disorder; chronic liver disease;  
KW circulatory disorder; heart failure; neurodegenerative disease;  
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;  
KW neurite outgrowth.  
XX  
XX Mus musculus.  
XX  
XX US6432673-B1.  
XX  
XX PD 13-AUG-2002.  
XX  
XX PF 07-DEC-1999; 99US-0457066.  
XX  
XX PR 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142576P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KB;  
PI Gilbertson DG, West JW;  
XX  
XX WPI; 2002-689759/74.  
DR N-PSDB; ABS68648.  
XX  
XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,  
PT ulcers, burns, skin grafting, female reproductive tract disorders,  
PT Parkinson's disease, and Alzheimer's disease -  
XX  
XX Example 4; Fig 2; 69pp; English.  
XX  
XX The invention relates to an isolated polypeptide, designated zvegf3  
CC (a vascular endothelial growth factor-like protein) of 111-136 amino acid  
CC residues in length and comprises the sequence appearing as ABG92889  
CC from amino acid residues 235-345. Also included are an isolated  
CC protein comprising a first polypeptide disulphide bonded to a second  
CC polypeptide, where each of the first and second polypeptides is from  
CC zvegf 3, and where the protein modulates cell proliferation,  
CC differentiation, metabolism or migration, the zvegf 3 encoding  
CC polynucleotides and zvegf 3 expression vectors and host cells  
CC zvegf 3 is useful as additives in tissue adhesives for promoting the  
CC revascularisation of the healing tissue, for designing molecules that  
CC antagonise semaphorin-stimulated activities, including neurite growth,  
CC cardiovascular development, cartilage and limb development, and T and  
CC B-cell function, and for imaging tumours or other sites of abnormal cell  
CC proliferation and in gene therapy applications. The proteins are useful  
CC therapeutically to stimulate tissue development or repair, or cellular  
CC differentiation or proliferation, for stimulating the growth of  
CC fibroblast or smooth muscle cells, as molecular weight standards, as  
CC reagents in assays for determining circulatory level of the protein or as  
CC standards in the analysis of cell phenotype, for identifying inhibitors  
CC of their activity which are useful for reducing the growth of solid  
CC tumours, for treating diabetic retinopathy, psoriasis, rheumatoid  
CC arthritis, various forms of cancers, autoimmune disease, inflammation,

CC myocardial ischaemia, scleroderma, and reducing fibrosis, including scar  
CC formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis,  
CC asbestosis), kidney fibrosis (including diabetic nephropathy),  
CC glomerulosclerosis, atherosclerosis, skin wounds, ulcers, burns, skin  
CC grafting, and female reproductive tract disorders, chronic liver disease  
CC (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory  
CC disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac  
CC sclerosis, neurodegenerative diseases such as multiple sclerosis,  
CC Parkinson's disease, Alzheimer's disease, and for regenerating neurite  
CC outgrowths following strokes. The gene for mouse zveg3 is located on  
CC chromosome 3. The present sequence represents zveg3.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLLGLLLLSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVVITISNGSIHS 60  
Db 1 MLLGLLLLSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVVITISNGSIHS 60  
Qy 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEVEEPPSDGSVL 120  
Db 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEVEEPPSDGSVL 120  
Qy 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Qy 181 LSDDLNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
Qy 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
Qy 301 VTKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRNAGG 345  
Db 301 VTKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 6  
AAB47890  
ID AAB47890 standard; Protein; 345 AA.  
XX  
AC AAB47890;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
XX Mouse zveg3.  
XX Human; mouse; zveg3; zveg4; platelet derived growth factor;  
KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;  
KW osteoblast; chondrocyte; bony defect; fracture; bone graft;  
KW implant; periodontal pocket; osteoclast; bone marrow stem cell;  
KW osteoporosis.  
XX  
OS Mus musculus.  
XX  
XX US2002004225-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 29-MAR-2001; 2001US-0823033.  
XX  
XX 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142576P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
PR 31-MAR-2000; 2000US-193723P.  
PR 07-DEC-1999; 99US-0457066.

XX (HART/) HART C E.  
PA (GILB/) GILBERTSON D G.  
XX  
XX Hart CE, Gilbertson DG;  
XX  
XX WPI; 2002-171026/22.  
DR N-PSDB; AAI72444.  
XX  
XX Promoting growth of bone, ligament or cartilage in a mammal, involves  
XX administering to the mammal a protein which comprises growth factor  
XX domain of zveg3 protein, a homolog of platelet-derived growth factor  
XX  
XX  
XX Claim 1; Page 19-20; 31pp; English.  
XX  
XX The sequences given in AAB47890 represent human and mouse zveg3,  
XX respectively. zveg3 is a platelet derived growth factor (PDGF) homolog  
XX and it was used in the method of the invention for promoting growth of  
XX bone, ligament or cartilage and stimulating proliferation of osteoblasts  
XX or chondrocytes in a mammal. The proteins used were preferably a dimeric  
XX protein of residues 235-345 of human zveg3 or all of the mouse zveg3  
XX protein, with a delivery vehicle. The method of the invention is useful  
XX for promoting growth of bone, ligament or cartilage in a mammal, where  
XX the composition is administered at a site of a bony defect, preferably  
XX a fracture, bone graft site, implant site, or periodontal pocket, and  
XX for stimulating proliferation of osteoblasts or chondrocytes in a  
XX mammal. It is further useful for promoting proliferation of osteoblasts,  
XX osteoclasts, chondrocytes or bone marrow stem cells, where the bone  
XX marrow stem cells are harvested from a patient prior to culture. The  
XX method is therefore useful for treating osteoporosis.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLLGLLLLSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVVITISNGSIHS 60  
Db 1 MLLGLLLLSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVVITISNGSIHS 60  
Qy 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEVEEPPSDGSVL 120  
Db 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEVEEPPSDGSVL 120  
Qy 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Qy 181 LSDDLNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
Qy 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
Qy 301 VTKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRNAGG 345  
Db 301 VTKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 7  
AAE13213  
ID AAE13213 standard; Protein; 345 AA.  
XX  
AC AAE13213;  
XX  
DT 12-FEB-2002 (first entry)  
XX  
DE Mouse platelet-derived growth factor (PDGF-C) protein.  
XX

KW Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;  
 KW cardiac hypertrophy; fibrosis.

OS Mus sp.

PN WO200172132-A1.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US09855.

XX 28-MAR-2000; 2000US-192507P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Eriksson U, Li X, Ponten A, Aase K, Li H;

XX WPI; 2002-010700/01.

XX A transgenic animal over-expressing platelet derived growth factor C is  
 PT useful to study and find therapy for disease associated with PDGF-C  
 PT over-expression, including cardiac hypertrophy and fibrosis -

PS Example 4; Page 42-43; 48pp; English.

XX The patent discloses a method for producing a transgenic, non-human  
 CC animal over-expressing a platelet derived growth factor C (PDGF-C),  
 CC or its functional fragment or analogue. The method involves introducing  
 CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing  
 CC the cell into a non-human animal and allowing the cell to develop into  
 CC a transgenic, non-human animal. The transgenic animal is useful as a  
 CC model to study disease states characterised by over-expression of PDGF-C  
 CC and to find therapy for those diseases, particularly hypertrophy and  
 CC fibrosis in various organs including the heart. The present sequence  
 CC is PDGF-C protein from mouse.

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4e-182;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLLGLLLLSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVRVTISGNSIHS 60  
 Db 1 MLLGLLLLSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHVRVTISGNSIHS 60  
 QY 61 PKPPTYPRNNVLVRLVAVDENVRIQLTFDERFGLDPEDDICKYDFVVEEESDGSVL 120  
 Db 61 PKPPTYPRNNVLVRLVAVDENVRIQLTFDERFGLDPEDDICKYDFVVEEESDGSVL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
 Db 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
 QY 181 LSLDLLNNAVTAFTLEELRYLEPDRAWQVLDLSLYKPTWQLLGKAFYLGKSKVNLNL 240  
 Db 181 LSLDLLNNAVTAFTLEELRYLEPDRAWQVLDLSLYKPTWQLLGKAFYLGKSKVNLNL 240  
 QY 241 LKEEVLKYSTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
 Db 241 LKEEVLKYSTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
 QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEECDCVCRNAGG 345  
 Db 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEECDCVCRNAGG 345

RESULT 8

ID ABG76398

XX ABG76398 standard; Protein; 345 AA.

AC ABG76398;

XX

DT 22-MAY-2003 (first entry)  
 XX Mouse growth factor homologue, zveg3.  
 XX  
 KW Mouse; growth factor homologue; zveg3; fibroblast; smooth muscle cell;  
 KW cell-surface platelet-derived growth factor alpha receptor; PDGF;  
 KW full-thickness skin wound; female reproductive tract; duodenal ulcer;  
 KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;  
 KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;  
 KW chronic active hepatitis; hepatic chronic passive congestion; stroke;  
 KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;  
 KW portal vein thrombosis; cardiac sclerosis; new vessel formation;  
 KW endothelial precursor stem cell; neovascularisation; wound healing;  
 KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;  
 KW sensory neurite outgrowth; brain damage; head injury; paralysis;  
 KW spinal injury; neurodegenerative disease; diabetic retinopathy;  
 KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;  
 KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;  
 KW proliferative vascular disorder; ocular neovascularisation;  
 KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;  
 KW angiogenesis; nervous system disorder; cytostatic; hepatotropic;  
 KW vulnary; tranquilliser; cerebroprotective; neuroprotective; nootropic;  
 KW ophthalmological; dermatological; coagulant; cardiac.  
 XX Mus musculus.  
 OS  
 XX US2002177193-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 02-MAY-2002; 2002US-0139583.  
 XX  
 XX 07-DEC-1998; 98US-111173P.  
 XX 06-JUL-1999; 99US-142576P.  
 XX 21-OCT-1999; 99US-161653P.  
 XX 12-NOV-1999; 99US-185255P.  
 XX 07-DEC-1999; 99US-04527066.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
 XX Gilbertson DG, West JW;  
 PI  
 PI WPI; 2003-328485/31.  
 DR N-PSDB; ABX93182.  
 DR  
 XX New isolated zveg3 polypeptide, useful for treating cancer.  
 PT Alzheimer's disease, Parkinson's disease, chronic active hepatitis,  
 PT hepatic vein thrombosis, comprises growth factor domain and CUB domain  
 PT  
 PS Claim 1; Fig 6; 73pp; English.  
 XX  
 XX The present invention relates to the isolation of a growth factor  
 CC homologue referred to as zveg3, and the polynucleotide sequence  
 CC encoding it. The zveg3 polypeptide is useful for stimulating the  
 CC growth of fibroblasts or smooth muscle cells, or for activating a  
 CC cell-surface platelet-derived growth factor (PDGF) alpha receptor.  
 CC The zveg3 polypeptide is useful as a PDGF alpha receptor agonist and  
 CC thus is useful for treating full-thickness skin wounds, female  
 CC reproductive tract and prolonged bleeding, periodontal disease,  
 CC damaged liver tissue, and duodenal ulcers. The polypeptide is also  
 CC useful as an additive in tissue adhesives for promoting  
 CC revascularisation of healing tissue. The zveg3 polypeptide is also  
 CC useful for treating liver damage including damage due to liver  
 CC disease, chronic active hepatitis, hepatic chronic passive congestion  
 CC (CPC), central haemorrhagic necrosis (CHN), hepatic vein thrombosis,  
 CC portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis.  
 CC The polypeptide is useful for enhancing expansion and mobilisation of  
 CC endothelial precursor stem cells, creating and stabilising new vessel  
 CC formation in areas requiring neovascularisation, including areas of  
 CC ischaemia, organ transplants, wound healing, and tissue grafting. It  
 CC may be used for treating peripheral neuropathies by increasing spinal

cord and sensory neurite outgrowth, and as part of therapeutic treatment for the regeneration of neurite outgrowths following strokes, brain damage caused by head injuries, and paralysis caused by spinal injuries. Application may also be made in treating neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease, Parkinson's disease), diabetic retinopathy, psoriasis, arthritis, scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds vgef3 is useful for blocking the mitogenic, chemotactic, or angiogenic effects of vgef3, and for treating proliferative vascular disorders, ocular neovascularisation, inflammatory disorders, rheumatoid arthritis, psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis, and diseases of the nervous system. The present sequence represents mouse vgef3.

XX SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 24; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISGNGSIHS 60  
Db 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISGNGSIHS 60  
QY 61 PKFPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLDEPDDEDDICKYDFVEVEPSPDGSVL 120  
Db 61 PKFPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLDEPDDEDDICKYDFVEVEPSPDGSVL 120  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPVLPPSS 180  
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPVLPPSS 180  
QY 181 LSLDLLNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LSLDLLNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVLEHHBECDVCVRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHLSLTDVLEHHBECDVCVRGNAGG 345

RESULT 9  
ID AAY33679 standard; Protein; 345 AA.  
XX AC AAY33679;  
XX XX 11-JAN-2000 (first entry)  
XX DT Human VEGF-E protein.  
XX DE VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
KW treatment; cardiovascular disorder; endothelial disorder; therapy;  
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
KW angiogenic disorder; age-related macular degeneration; vascular disease;  
KW neovascularization; tumor; gene mapping.  
XX OS Homo sapiens.  
XX XX WO9947677-A2.  
XX XX 23-SEP-1999.  
XX XX 10-MAR-1999; 99WO-US05190.  
XX XX 17-MAR-1998; 98US-0040220.  
XX PR 02-NOV-1998; 98US-0184216.

PA (GETH ) GENENTECH INC.  
XX Ferrara N, Kuo SS;  
XX WPI; 1999-580306/49.  
DR N-PSDB; AAZ23691.  
XX New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy -  
XX Claim 1; Fig 2; 122pp; English.  
XX This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquilizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy. It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.

XX SQ Sequence 345 AA;  
Query Match 90.2%; Score 1667; DB 20; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISGNGSIHS 60  
Db 1 MSLFGLLLTSALAGORQQAESNLSSKFQFSNKEQNGVQDPOHERIITVTNGSIHS 60  
QY 61 PKFPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLDEPDDEDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPHTYPRNTVLVRLVAVDENVVWQLTFDERFGLDEPDDEDDICKYDFVEVEPSPDGSVL 120  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPVLPPSS 180  
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPVLPPSS 180  
QY 181 LSLDLLNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LPDLDLNNATFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFVFGKSRVDLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVLEHHBECDVCVRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHLSLTDVLEHHBECDVCVRGNAGG 345  
RESULT 10  
AAY41766



Db 61 PRFPHTYPRNTVLVWRLVAEENVMQLTDFDERFGLDEPDDICKYDFVEEPPSDGTIL 120  
QY 121 GRWCGSGTVPGKOTSGKNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTAEVSFVLPPSA 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPLDLINNAITAFSTLEDLIRYLEPERWQLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVGRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 11  
AAV30023  
ID AAV30023 standard; Protein; 345 AA.  
XX  
AC AAV30023;  
XX  
DT 11-OCT-1999 (first entry)  
XX  
DE Human vascular endothelial growth factor related protein.  
XX  
KW Vascular endothelial growth factor related protein; VEGF-R protein;  
KW tissue growth inhibition; tumour growth; cancer; tissue growth;  
KW angiogenesis; coronary artery blockage.  
XX  
OS Homo sapiens.  
XX  
FN WO9937671-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 26-JAN-1999; 99WO-US01574.  
XX  
PR 31-AUG-1998; 98US-0098548.  
PR 27-JAN-1998; 98US-0072635.  
PR 05-JUN-1998; 98US-008089.  
PR 24-JUN-1998; 98US-0090544.  
XX  
PA (ELIL) LILLY & CO ELI.  
XX  
PI Dou S, Na S, Song HY;  
XX  
DR WPI; 1999-458680/38.  
DR N-PSDB; AAV86352.

XX A vascular endothelial growth factor related protein and related  
PT polynucleotide, useful for identifying antagonists and binding  
PT compounds

XX Claim 1; Page 56-58; 62pp; English.  
XX  
XX The present sequence represents a vascular endothelial growth factor  
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify  
CC compounds that bind to it or that antagonize its activity. VEGF-R  
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting  
CC tissue growth. This is useful for inhibiting tumour growth and for  
CC treating cancer. VEGF-R itself can be used to stimulate tissue  
CC growth, angiogenesis and to treat coronary artery blockage. The  
CC VEGF-R coding sequence can be used for the recombinant production of  
CC the VEGF-R protein.  
XX

SQ Sequence 345 AA;  
Query Match 90.2%; Score 1667; DB 20; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLITLSALAGQRTGTRAESNLSSKLQLSSDKQNGVQDPRHERVVTISGNGSIHS 60  
Db 1 MSLFGLLLITLSALAGQRTGTRAESNLSSKQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60  
QY 61 PRFPHTYPRNTVLVWRLVAEENVMQLTDFDERFGLDEPDDICKYDFVEEPPSDGTIL 120  
Db 61 PRFPHTYPRNTVLVWRLVAEENVMQLTDFDERFGLDEPDDICKYDFVEEPPSDGTIL 120  
QY 121 GRWCGSGTVPGKOTSGKNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYNVMPQFTAEVSFVLPPSA 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPLDLINNAITAFSTLEDLIRYLEPERWQLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVGRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 12  
AAB48657  
ID AAB48657 standard; Protein; 345 AA.  
XX  
AC AAB48657;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Human zvegfg3, SEQ ID NO:33.  
XX  
KW Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;  
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;  
KW neovascularisation; tissue repair; proliferation; differentiation;  
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;  
KW periodontal disease; bone fracture; wound healing; vulnarary; ischaemia;  
KW immunomodulation; hepatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200066736-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US40047.  
XX  
PR 03-MAY-1999; 99US-0304216.  
PR 10-NOV-1999; 99US-0164463.  
PR 04-FEB-2000; 2000US-0180169.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX  
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
XX  
XX WPI; 2000-687541/67.  
XX N-PSDB; AAC81582.

XX Growth factor homologs and the nucleic acids that encode them, useful  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease -  
XX  
XX Claim 48; Page 125-126; 143pp; English.

XX The invention relates to the human growth factor homologue zvegfg4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)

characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zveg4 or fragments thereof, particularly human zveg4/human zveg3 fusions; expression constructs and host cells comprising human zveg4 nucleic acids; the recombinant expression of human zveg4; an antibody which binds to human zveg4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zveg4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zveg4-derived polypeptides; and a method of detecting a genetic abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zveg3.

XX Sequence 345 AA;  
Query Match 90.2%; Score 1667; DB 21; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MSFLGILLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMLVWRLVAVDENVRQLTDFRERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
Db 61 PKPHTYPRNMLVWRLVAVDENVRQLTDFRERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTSPSVLPSS 180  
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTSPSVLPSS 180  
QY 181 LSJDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 13  
AAB24250  
ID AAB24250 standard; Protein; 345 AA.  
AC AAB24250;  
XX  
XX  
XX 08-FEB-2001 (first entry)  
XX Human platelet-derived growth factor related protein LP8.  
XX Human; platelet derived growth factor related protein; LP8; VEGFh;  
KW vascular endothelial growth factor h; tissue regeneration; vulnerary;  
KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX  
XX WO200059940-A2.  
PN

XX 12-OCT-2000.  
XX 24-MAR-2000; 2000WO-US06427.  
XX 06-APR-1999; 99US-0127913.  
XX (ELIL) LILLY & CO ELI.  
XX Hammond LJ, Na S;  
XX WPI; 2000-664991/64.  
XX N-PSDB; AAC64426.  
XX Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist  
XX Claim 4; Page 63-64; 64pp; English.  
XX The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LP8 or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LP8 antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LP8 are useful for treating atherosclerosis. The present sequence represents human LP8, which is also called VEGFh.

XX Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 21; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MSFLGILLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMLVWRLVAVDENVRQLTDFRERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
Db 61 PKPHTYPRNMLVWRLVAVDENVRQLTDFRERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTSPSVLPSS 180  
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTSPSVLPSS 180  
QY 181 LSJDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 14  
AAB44322  
ID AAB44322 standard; Protein; 345 AA.  
XX  
XX AAB44322;  
XX 08-FEB-2001 (first entry)  
XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.  
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;





CC vascularization. This sequence represents the RACE generated human VEGF-X  
CC protein described in the method of the invention.

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XX	Sequence	345 AA;
SQ		

AA	Sequence	345 AA;
SQ		

Query Match 90.2%; Score 1667; DB 21; Length 345;

Best Local Similarity 87.0%; Pred. No. 2.1e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

0v 1 MLLGLLLTSALAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60

[illegible]

Db 1 MSLFGLLLTTSALAGRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60

Qy 61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLDEPPEDDICKYDFVEVEEPSDGSVL 120

Case	Age	Sex	Occupation	Duration of illness	Site of lesion	Pathological changes	Microscopic findings	Diagnosis
1	25	M	Teacher	10 years	Brain	Chronic	...	...
2	35	F	Housewife	5 years	Brain	Chronic	...	...
3	45	M	Farmer	15 years	Brain	Chronic	...	...
4	55	F	Teacher	10 years	Brain	Chronic	...	...
5	65	M	Retired	20 years	Brain	Chronic	...	...
6	75	F	Housewife	15 years	Brain	Chronic	...	...
7	85	M	Retired	25 years	Brain	Chronic	...	...
8	95	F	Housewife	30 years	Brain	Chronic	...	...
9	105	M	Retired	35 years	Brain	Chronic	...	...
10	115	F	Housewife	40 years	Brain	Chronic	...	...
11	125	M	Retired	45 years	Brain	Chronic	...	...
12	135	F	Housewife	50 years	Brain	Chronic	...	...
13	145	M	Retired	55 years	Brain	Chronic	...	...
14	155	F	Housewife	60 years	Brain	Chronic	...	...
15	165	M	Retired	65 years	Brain	Chronic	...	...
16	175	F	Housewife	70 years	Brain	Chronic	...	...
17	185	M	Retired	75 years	Brain	Chronic	...	...
18	195	F	Housewife	80 years	Brain	Chronic	...	...
19	205	M	Retired	85 years	Brain	Chronic	...	...
20	215	F	Housewife	90 years	Brain	Chronic	...	...
21	225	M	Retired	95 years	Brain	Chronic	...	...
22	235	F	Housewife	100 years	Brain	Chronic	...	...
23	245	M	Retired	105 years	Brain	Chronic	...	...
24	255	F	Housewife	110 years	Brain	Chronic	...	...
25	265	M	Retired	115 years	Brain	Chronic	...	...
26	275	F	Housewife	120 years	Brain	Chronic	...	...
27	285	M	Retired	125 years	Brain	Chronic	...	...
28	295	F	Housewife	130 years	Brain	Chronic	...	...
29	305	M	Retired	135 years	Brain	Chronic	...	...
30	315	F	Housewife	140 years	Brain	Chronic	...	...
31	325	M	Retired	145 years	Brain	Chronic	...	...
32	335	F	Housewife	150 years	Brain	Chronic	...	...
33	345	M	Retired	155 years	Brain	Chronic	...	...
34	355	F	Housewife	160 years	Brain	Chronic	...	...
35	365	M	Retired	165 years	Brain	Chronic	...	...
36	375	F	Housewife	170 years	Brain	Chronic	...	...
37	385	M	Retired	175 years	Brain	Chronic	...	...
38	395	F	Housewife	180 years	Brain	Chronic	...	...
39	405	M	Retired	185 years	Brain	Chronic	...	...
40	415	F	Housewife	190 years	Brain	Chronic	...	...
41	425	M	Retired	195 years	Brain	Chronic	...	...
42	435	F	Housewife	200 years	Brain	Chronic	...	...
43	445	M	Retired	205 years	Brain	Chronic	...	...
44	455	F	Housewife	210 years	Brain	Chronic	...	...
45	465	M	Retired	215 years	Brain	Chronic	...	...
46	475	F	Housewife	220 years	Brain	Chronic	...	...
47	485	M	Retired	225 years	Brain	Chronic	...	...
48	495	F	Housewife	230 years	Brain	Chronic	...	...
49	505	M	Retired	235 years	Brain	Chronic	...	...
50	515	F	Housewife	240 years	Brain	Chronic	...	...
51	525	M	Retired	245 years	Brain	Chronic	...	...
52	535	F	Housewife	250 years	Brain	Chronic	...	...
53	545	M	Retired	255 years	Brain	Chronic	...	...
54	555	F	Housewife	260 years	Brain	Chronic	...	

Db 61 PRFPHTYPRNTVLVWRLVAVEENVWQLTTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120

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QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFFPSEPGFCIHYSIIMPQVETISPSVLPSS 180

[illegible]

D6 121 GRWCGSGTVPGRQISKGNQIRIRFVSDEYFFPSEFGCIHYNIVMPQFT EAVSPSVLPFSA 180

101 TGTDTYNTAETSTFETTPVTEPPPEWMTDSTVKPTWOTLCKAEIYCKKSKVTNTNT. 240

Search completed: November 25, 2003, 21:02:15

Job time : 36.9375 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:00:19 ; Search time 13.006 seconds  
(without alignments)  
1122.351 Million cell updates/sec

Title: US-09-852-209A-7  
Perfect score: 1848  
Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHECDVCRCNAGG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1848	100.0	345	4	US-09-457-066-43
2	1848	100.0	345	4	US-09-564-595D-35
3	1848	100.0	345	4	US-09-706-968-43
4	1667	90.2	345	4	US-09-040-220D-2
5	1667	90.2	345	4	US-09-457-066-2
6	1667	90.2	345	4	US-09-265-686-2
7	1667	90.2	345	4	US-09-540-224-5
8	1667	90.2	345	4	US-09-564-595D-33
9	1667	90.2	345	4	US-09-706-968-2
10	1204.5	65.2	303	4	US-09-564-595D-57
11	1200	64.9	302	4	US-09-564-595D-54
12	1035.5	56.0	317	4	US-09-564-595D-56
13	1019	55.1	316	4	US-09-564-595D-55
14	752	40.7	370	4	US-09-457-066-37
15	752	40.7	370	4	US-09-540-224-2
16	752	40.7	370	4	US-09-564-595D-2
17	752	40.7	370	4	US-09-706-968-37
18	746.5	40.4	370	4	US-09-540-224-4
19	746.5	40.4	370	4	US-09-564-595D-53
20	185	10.0	1015	4	US-09-285-385C-2
21	183	9.9	1012	4	US-09-285-385C-4
22	181	9.8	788	1	US-08-572-225-1
23	181	9.8	986	4	US-09-285-385C-19
24	177.5	9.6	730	3	US-08-872-757-2
25	177.5	9.6	730	4	US-09-850-048A-2
26	175	9.5	101	3	US-09-374-135-6
27	172	9.3	922	4	US-09-116-473-4

28	169	9.1	923	3	US-08-936-135-6	Sequence 6, Appli
29	168	9.1	986	3	US-08-872-757-4	Sequence 4, Appli
30	168	9.1	986	3	US-09-850-048A-4	Sequence 4, Appli
31	165	8.9	1013	2	US-08-866-650-3	Sequence 3, Appli
32	165	8.9	1013	2	US-09-021-287-3	Sequence 3, Appli
33	165	8.9	1013	3	US-09-240-473-3	Sequence 3, Appli
34	162	8.8	591	3	US-08-991-408-4	Sequence 4, Appli
35	162	8.8	591	4	US-09-432-473-4	Sequence 4, Appli
36	162	8.8	1013	2	US-08-866-650-5	Sequence 5, Appli
37	162	8.8	1013	2	US-09-021-287-5	Sequence 5, Appli
38	162	8.8	1013	3	US-08-991-408-2	Sequence 2, Appli
39	162	8.8	1013	3	US-09-240-473-5	Sequence 5, Appli
40	162	8.8	1013	4	US-09-432-473-2	Sequence 2, Appli
41	162	8.8	1013	4	US-09-285-385C-20	Sequence 20, Appli
42	158	8.5	449	2	US-08-839-008-2	Sequence 2, Appli
43	158	8.5	449	2	US-08-839-008-9	Sequence 9, Appli
44	158	8.5	3623	4	US-09-341-461-2	Sequence 2, Appli
45	156.5	8.5	111	4	US-09-341-461-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1  
US-09-457-066-43  
; Sequence 43, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-457-066-43

Query Match	100.0%;	Score 1848;	DB 4;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 7.2e-195;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLLGLLLLTALAGQRTGTTRASNLSKQLQSSDKEQNGVQDP	PRHVRVTTISG	NGSIHS 60
Db	1	MLLGLLLLTALAGQRTGTTRASNLSKQLQSSDKEQNGVQDP	PRHVRVTTISG	NGSIHS 60
Qy	61	PKPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLED	PDDICKYDFVEVEE	PSDGSVL 120
Db	61	PKPHTYPRNMVLVRLVAVDENVRIQLTFDERFGLED	PDDICKYDFVEVEE	PSDGSVL 120
Qy	121	GRWCGSGTVPGKOTSGKNHRIIRFVSDVEYFPSPGFCIHYS	IIMPQVTTETTS	PSVLPSS 180
Db	121	GRWCGSGTVPGKOTSGKNHRIIRFVSDVEYFPSPGFCIHYS	IIMPQVTTETTS	PSVLPSS 180
Qy	181	LSLDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAF	LYGKSKVNNLN	240
Db	181	LSLDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAF	LYGKSKVNNLN	240
Qy	241	LKEEVKLYSCTPRNFSVSIREEKRTDTTIFWPGCLLVKRCGNCA	CCLHNCBQCQVPRK	300
Db	241	LKEEVKLYSCTPRNFSVSIREEKRTDTTIFWPGCLLVKRCGNCA	CCLHNCBQCQVPRK	300
Qy	301	VTKKHEVQLRPKTVGKLHSLTDVALEHHEECDCVCRNAGG	345	

Db 301 VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 2

US-09-564-595D-35  
; Sequence 35, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-564-595D-35

Query Match 100.0%; Score 1848; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 7.2e-195;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRRVVTISGNGSIHS	60
Db	1	MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRRVVTISGNGSIHS	60
QY	61	PKFPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120
Db	61	PKFPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120
QY	121	GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS	180
Db	121	GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS	180
QY	181	LSLDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNNLNL	240
Db	181	LSLDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNNLNL	240
QY	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPRK	300
Db	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPRK	300
QY	301	VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345	
Db	301	VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345	

## RESULT 3

US-09-706-968-43  
; Sequence 43, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968

; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-706-968-43

QY	1	MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRRVVTISGNGSIHS	60
Db	1	MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRRVVTISGNGSIHS	60
QY	61	PKFPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120
Db	61	PKFPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120
QY	121	GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS	180
Db	121	GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS	180
QY	181	LSLDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNNLNL	240
Db	181	LSLDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNNLNL	240
QY	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPRK	300
Db	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPRK	300
QY	301	VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345	
Db	301	VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345	

## RESULT 4

US-09-040-220D-2  
; Sequence 2, Application US/09040220D  
; Patent No. 6391311  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION  
; FILE REFERENCE: P1122  
; CURRENT APPLICATION NUMBER: US/09/040,220D  
; CURRENT FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Human  
US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY	1	MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVODPRHRRVVTISGNGSIHS	60
Db	1	MSLFGLLLTTSALAGORQTQAEESNLSSKQFSSNKQNGVODPRHRIITVTNGSIHS	60
QY	61	PKFPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120
Db	61	PRFPHTYPRNTVLVWRLVAVENVQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL	120

QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFYKSKVYNLNL 240  
Db 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFYKSKVYNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

## RESULT 5

US-09-457-066-2  
Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Gao, Zeren  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Shoemaker, Kimberly E.  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: West, James W.  
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
FILE REFERENCE: 98-60  
CURRENT APPLICATION NUMBER: US/09/457,066  
CURRENT FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-457-066-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTALSAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISNGSIHS 60  
Db 1 MSLFGLLLTALSAGQRTGTRAESNLSSKQFQSSNKEQNGVQDPRHVRVVTISNGSIHS 60  
QY 61 PKFPHYPRNMVWLVWRLVAVDENVRIQLTFDRFGLDEDDICKYDFVEVEEPPSDGTVL 120  
Db 61 PRFPHYPRNTVLWRLVAEENVWVQLTFDRFGLDEDDICKYDFVEVEEPPSDGTVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFYKSKVYNLNL 240  
Db 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFYKSKVYNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

## RESULT 6

US-09-265-686-2  
Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Patent No. 6455283  
GENERAL INFORMATION:  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Kuo, Sophia S.  
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
FILE REFERENCE: P1122P2  
CURRENT APPLICATION NUMBER: US/09/265,686  
CURRENT FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: US 09/040,220  
PRIOR FILING DATE: 1998-03-17  
PRIOR APPLICATION NUMBER: US 09/184,216  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 2  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Human  
US-09-265-686-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTALSAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISNGSIHS 60  
Db 1 MSLFGLLLTALSAGQRTGTRAESNLSSKQFQSSNKEQNGVQDPRHVRVVTISNGSIHS 60  
QY 61 PKFPHYPRNMVWLVWRLVAVDENVRIQLTFDRFGLDEDDICKYDFVEVEEPPSDGTVL 120  
Db 61 PRFPHYPRNTVLWRLVAEENVWVQLTFDRFGLDEDDICKYDFVEVEEPPSDGTVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFYKSKVYNLNL 240  
Db 181 LSLDLLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLKGAFYKSKVYNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVQLRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

## RESULT 7

US-09-540-224-5  
Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: Hart, Charles E.  
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4  
FILE REFERENCE: 00-28  
CURRENT APPLICATION NUMBER: US/09/540,224  
CURRENT FILING DATE: 2000-03-31  
EARLIER APPLICATION NUMBER: US 60/180,169  
EARLIER FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-540-224-5

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVDPQPRHVRVVTISNGSIHS 60  
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVDPQPRHVRVVTISNGSIHS 60  
QY 61 PKPPTYPRNMVLMVRLVAVDENVRVQLTDFERFGLDEDDICKYDFVEVEBPSDGSVL 120  
Db 61 PRPPTYPRNTVLMVRLVAVDENVRVQLTDFERFGLDEDDICKYDFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPGKOTSGKNHRIIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFVGRKSRVDNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 8

US-09-564-595D-33  
; Sequence 33, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-564-595D-33

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVDPQPRHVRVVTISNGSIHS 60  
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVDPQPRHVRVVTISNGSIHS 60  
QY 61 PKPPTYPRNMVLMVRLVAVDENVRVQLTDFERFGLDEDDICKYDFVEVEBPSDGSVL 120  
Db 61 PRPPTYPRNTVLMVRLVAVDENVRVQLTDFERFGLDEDDICKYDFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPGKOTSGKNHRIIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFVGRKSRVDNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300

Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 9

US-09-706-968-2  
; Sequence 2, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; PRIOR FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-706-968-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVDPQPRHVRVVTISNGSIHS 60  
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVDPQPRHVRVVTISNGSIHS 60  
QY 61 PKPPTYPRNMVLMVRLVAVDENVRVQLTDFERFGLDEDDICKYDFVEVEBPSDGSVL 120  
Db 61 PRPPTYPRNTVLMVRLVAVDENVRVQLTDFERFGLDEDDICKYDFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPGKOTSGKNHRIIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFVGRKSRVDNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 10

US-09-564-595D-57  
; Sequence 57, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19

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US-09-564-595D-54
Query Match 64.9%; Score 1200; DB 4; Length 302;
Best Local Similarity 72.4%; Pred. No. 1.4e-123;
Matches 215; Conservative 35; Mismatches 43; Indels 4; Gaps 2

QY 46 HERVVTISNGSIHSPKPHPTYPNNMLVWRLVAVDENVRVQLTDFERFGLDEPDDICK 105
DB 1 HERIITVTNGSIHSPRPHPTYPNNMLVWRLVAVDENVRVQLTDFERFGLDEPDDICK 60
QY 106 YDFVEVEEPSDGVSLGRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMP 165
DB 61 YDFVEVEEPSDGTILGRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMP 120
QY 166 QVTETTPSVLPSPSSLSLDLNNAVTAFSTLEELIRYLEPRQWQVLDLSLYKPTWQLLKG 225
DB 121 QPTEAVSPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEPERWQVLDLDRPTWQLLKG 180
QY 226 AFLYKKSQVNNLLKSEVKLYSCTPRNFSVSIREEELKRTDTTFWPCGLLVKRCGNCA 285
DB 181 AFVFGKRS-VDLRLNDDAKRYSTPRNFSVNIREEELKANVVFPPRCCLLVQRCGGNGC 239
QY 286 CCLHNCNEQCQVPRKVTKKYHEVLQRLP---KTGVKGLHKSITDVALEHHEECDCVC 339
DB 240 CGTVNWRSTCNSGKTVKKYHEVLQFPQGHKRGRAKTMALVDIQLDHERCDDIC 296

RESULT 12
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match 56.0%; Score 1035.5; DB 4; Length 317;
Best Local Similarity 60.2%; Pred. No. 2e-105;
Matches 192; Conservative 47; Mismatches 57; Indels 23; Gaps 6

QY 47 ERVVTISNGSIHSPKPHPTYPNNMLVWRLVAVDENVRVQLTDFERFGLDEPDDICKY 106
DB 2 DETIQVKGNGYVQSPRFPNPSYPRNLLTWRLHS-QENTRIQLVFNQFGLAEANDICRY 60
QY 107 DFVEVEEPSDGVSL--GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSII- 163
DB 61 DFVEVEDISETTIIRGRWCGHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYISLLE 120
QY 164 --MPQVTETT-----SPSVLPSSLSLDLNNAVTAFSTLEELIRYLEPRD 206
DB 121 DFQPAASSETNWESVTSSISGVSYNPSVTDPT-LIIADLKKIAEFTVEDLLKYFNP 179
QY 207 RQVQDLSLYKPTWQLLKGAFLYGKSKVNNLLKSEVKLYSCTPRNFSVSIREEELKRT 266

US-09-564-595D-54
Query Match 65.2%; Score 1204.5; DB 4; Length 303;
Best Local Similarity 71.3%; Pred. No. 4.5e-124;
Matches 216; Conservative 42; Mismatches 40; Indels 5; Gaps 3;

QY 47 ERVVTISNGSIHSPKPHPTYPNNMLVWRLVAVDENVRVQLTDFERFGLDEPDDICKY 106
DB 2 DETIQVKGNGYVQSPRFPNPSYPRNLLTWRLHS-QENTRIQLVFNQFGLAEANDICRY 60
QY 107 DFVEVEEPSDGVSL--GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSII- 163
DB 61 DFVEVEDISETTIIRGRWCGHKEVPPRIKSTNQIKITFKSDDYFVAKPGFKIYISLLE 120
QY 164 --MPQVTETTPSVLPSPSSLSLDLNNAVTAFSTLEELIRYLEPRQWQVLDLSLYKPTWQL 222
DB 121 DFQPAASVSPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEPERWQVLDLDRPTWQL 180
QY 223 LGKAFLYGKSKVNNLLKSEVKLYSCTPRNFSVSIREEELKRTDTTFWPCGLLVKRCGG 282
DB 181 LGKAFVFGKRSVVDLNLLETVRIYLSCTPRNFSVSIREEELKRTDTTFWPCGLLVKRCGG 240
QY 283 NCACCLHNCNEQCQVPRKVTKKYHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGN 342
DB 241 NCACCLHNCNEQCQVPSKVTKKYHEVLQRLPKTGVRLHKSITDVALEHHEECDCVCRGS 300
QY 343 AGG 345
DB 301 TGG 303

RESULT 11
US-09-564-595D-54
; Sequence 54, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide

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180 SWQEDLENNYLDTPRYGRSY-HDRKSKVVDLNNLLTEEVRLYSCTPRNFSVIREELKRT 238  
QY 267 DTIFWPGCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRPKTKYKGLHSLTD 326  
Db 239 DTIFWPGCLLVKRCGNCACCLHNCOCVPSKTKYKHYEVLQRPKTKYKGLHSLTD 298  
QY 327 VALEHHEECDCVCRGNAGG 345  
Db 299 VALEHHEECDCVCRGSTGG 317  
RESULT 13  
US-09-564-595D-55  
; Sequence 55, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 55  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polypeptide  
US-09-564-595D-55  
Query Match 55.1%; Score 1019; DB 4; Length 316;  
Best Local Similarity 60.4%; Pred. No. 1.3e-103;  
Matches 189; Conservative 41; Mismatches 61; Indels 22; Gaps 5;  
QY 46 HERVVTISNGSIHSPKFPHTYPRNVLVRLVAVDENVRIQLTFDEFGLEDPEDDICK 105  
Db 1 HERIIVTNGSIHSPKFPHTYPRNVLVRLVAVDENVRIQLTFDEFGLEDPEDDICK 60  
QY 106 YDFVEVEEEDSGVLRGWSGTVPGKQTSKGNHIRIRFVSDYFPSEPGFCIHYIIMP 165  
Db 61 YDFVEVEEEDSGVLRGWSGTVPGKQTSKGNHIRIRFVSDYFPSEPGFCIHYIIMP 120  
QY 166 QVTET-----TSFVLPSPSSLSLIDLNNAVTAFTLEELIRYLEPDRWQ 209  
Db 121 QFTAEATNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDVLDLKYFNPESWQ 179  
QY 210 VLDLSYKPTQWLGLKAFYKSKSVNLLKEEVKLYSCTPRNFSVIREELKRTDTI 269  
Db 180 EDLENNYLDTPRYGRSY-HDRKSK-VDLDRNDDAKRYSCPTNYSVNIREEKLNAV 237  
QY 270 FWPGCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRP---KTGKGLHSLTD 326  
Db 238 FFPFRCCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRPFGHIKRRGRKTAVALVD 297  
QY 327 VALEHHEECDCVC 339  
Db 298 IQLDHHERCDIC 310  
RESULT 14  
US-09-457-066-37  
; Sequence 37, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:

APPLICANT: Gao, Zeren  
APPLICANT: Hart, Charles E.  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Shoemaker, Kimberly E.  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: West, James W.  
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
FILE REFERENCE: 98-60  
CURRENT APPLICATION NUMBER: US/09/457,066  
CURRENT FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 37  
LENGTH: 370  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-457-066-37  
Query Match 40.7%; Score 752; DB 4; Length 370;  
Best Local Similarity 45.3%; Pred. No. 4.3e-74;  
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;  
QY 37 RONGVOD-PRHERVTISNGSIHSPKFPHTYPRNVLVRLVAVDENVRIQLTFDEFG 95  
Db 42 ESNHLTDLYRDETITQVKGNGYVQSPRFPNSYPRNLLTWRLHS-QENTRIQLVFDNQG 100  
QY 96 LEDPEDDICKYDFVEVEEEDSGVLR---GRWCSGTVPGKQTSKGNHIRIRFVSDYFPSE 153  
Db 101 LREAENDICRYDFVEVEDISESTIIRGWSGTVPGKQTSKGNHIRIRFVSDYFPSE 160  
QY 154 PGFCIHYSI---MPQVTETT-----SPSVLPSPSSLSLIDLNNAVTAFTST 195  
Db 161 PGFKIYSLLEDFOPAASSETNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFT 219  
QY 196 LEELIRYLEPDRWQVLDLSYKPTQWLGLKAFYKSKSVNLLKEEVKLYSCTPRNF 255  
Db 220 VEDLLKYFNPESWQEDLENNYLDTPRYGRSY-HDRKSK-VDLDRNDDAKRYSCPTN 277  
QY 256 SVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRP-- 313  
Db 278 SVNIREELKLANVFFPRCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRPFGH 337  
QY 314 -KTGKGLHSLTDVALEHHEECDCVC 339  
Db 338 IKRGRKTAVALVDIQLDHHERCDIC 364  
RESULT 15  
US-09-540-224-2  
; Sequence 2, Application US/09540224  
; Patent No. 6468543  
; GENERAL INFORMATION:  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: Hart, Charles E.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; FILE REFERENCE: 00-28  
; CURRENT APPLICATION NUMBER: US/09/540,224  
; CURRENT FILING DATE: 2000-03-31  
; EARLIER APPLICATION NUMBER: US 60/180,169  
; EARLIER FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-540-224-2  
Query Match 40.7%; Score 752; DB 4; Length 370;  
Best Local Similarity 45.3%; Pred. No. 4.3e-74;  
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

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Qy 37 BONGVQD--PRHERVVITISGNGSIHSPKPPHTYPRNMVLVRLVAVDENVRQLTFDERFG 95
Db 42 ESNHLLDLYRDETIQVKGNGYVQSPRPNSYPRNLLITWRLHS-QENTRIQLVFDNQFG 100
Qy 96 LEDPEDDICKYDFVEVEPEPSPGVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPSE 153
Db 101 LEEAENDICRYDFVEVEDISETSTIIRGWCGHKEVPPRIKSRTNQIKITPKSDDYFVAK 160
Qy 154 PGFCIHYSII---MPQVTETT-----SPSVLPSPSLSLDLLNNAVTAFTST 195
Db 161 PGFKIYYSLLEDFQAAASETNWESVTSSISGVSYNSFSVTDTP-TLIADALDKKIAEFD 219
Qy 196 LEEELIRYLEPDRWQVDLSLYKPTWQLLGAFLYKSKSVNVLNLLKEEVKLYSCTPRNF 255
Db 220 VEDLLKYFNPSQWQEDLENMYLDTPRYGRSY-HDKSK-VDLDRINDDAKRYSC 277
Qy 256 SVSIREELKRTDTIIPWGCLLVRCGNCACCLHNCBQCQVPRKVTYKHYEVLQLRP-- 313
Db 278 SVNIREELKLANVFPFRCLLVQRCGNGCGGTVMNRSCNCGKTVKKHYEVLQFEPGH 337
Qy 314 -KTGVKGLHKSILTOVALEHHEECDCVC 339
Db 338 IRRGRAKTMALVDIQLDHHERCDCIC 364
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Search completed: November 25, 2003, 21:06:21  
Job time : 13.006 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:04:39 ; Search time 24.3006 Seconds  
(without alignments)  
2618.575 Million cell updates/sec

Title: US-09-852-209A-7

Perfect score: 1848

Sequence: 1 MLLGLLLTSALAGORTGT.....DVALEHHEHSCDVCVRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	9	US-09-823-033-4
2	1848	100.0	345	9	US-09-818-943-2
3	1848	100.0	345	10	US-09-852-209A-7
4	1848	100.0	345	14	US-10-139-583-43
5	1848	100.0	345	15	US-10-131-600-7
6	1848	100.0	345	15	US-10-264-361-4
7	1667	90.2	345	9	US-09-823-033-2
8	1667	90.2	345	9	US-09-923-995-4
9	1667	90.2	345	10	US-09-795-006A-149
10	1667	90.2	345	10	US-09-978-295A-488
11	1667	90.2	345	10	US-09-978-637-488
12	1667	90.2	345	10	US-09-978-192A-488
13	1667	90.2	345	11	US-09-999-832A-488
14	1667	90.2	345	11	US-09-978-189-488
15	1667	90.2	345	11	US-09-796-753-6

16	1667	90.2	345	11	US-09-978-608A-488	Sequence 488, App
17	1667	90.2	345	11	US-09-978-585A-488	Sequence 488, App
18	1667	90.2	345	11	US-09-978-191A-488	Sequence 488, App
19	1667	90.2	345	11	US-09-978-403A-488	Sequence 488, App
20	1667	90.2	345	11	US-09-978-564A-488	Sequence 488, App
21	1667	90.2	345	11	US-09-999-833A-488	Sequence 488, App
22	1667	90.2	345	11	US-09-981-915A-488	Sequence 488, App
23	1667	90.2	345	11	US-09-978-824-488	Sequence 488, App
24	1667	90.2	345	11	US-09-918-585A-488	Sequence 488, App
25	1667	90.2	345	11	US-09-978-423A-488	Sequence 488, App
26	1667	90.2	345	11	US-09-978-193A-488	Sequence 488, App
27	1667	90.2	345	11	US-09-999-830A-488	Sequence 488, App
28	1667	90.2	345	11	US-09-978-757A-488	Sequence 488, App
29	1667	90.2	345	11	US-09-978-187B-488	Sequence 488, App
30	1667	90.2	345	11	US-09-978-643A-488	Sequence 488, App
31	1667	90.2	345	12	US-09-978-375A-488	Sequence 488, App
32	1667	90.2	345	12	US-09-978-188A-488	Sequence 488, App
33	1667	90.2	345	12	US-09-978-298A-488	Sequence 488, App
34	1667	90.2	345	12	US-10-137-870-286	Sequence 286, App
35	1667	90.2	345	12	US-10-140-018-286	Sequence 286, App
36	1667	90.2	345	12	US-10-140-021-286	Sequence 286, App
37	1667	90.2	345	12	US-10-140-274-286	Sequence 286, App
38	1667	90.2	345	12	US-10-140-471-286	Sequence 286, App
39	1667	90.2	345	12	US-10-140-807-286	Sequence 286, App
40	1667	90.2	345	12	US-10-140-922-286	Sequence 286, App
41	1667	90.2	345	12	US-10-140-924-286	Sequence 286, App
42	1667	90.2	345	12	US-10-140-926-286	Sequence 286, App
43	1667	90.2	345	12	US-10-141-698-286	Sequence 286, App
44	1667	90.2	345	12	US-10-141-702-286	Sequence 286, App
45	1667	90.2	345	12	US-10-141-704-286	Sequence 286, App

#### ALIGNMENTS

RESULT 1  
US-09-823-033-4  
; Sequence 4, Application US/09823033  
; Patent No. US2002004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-823-033-4

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5,8e-174;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLLGLLLTSALAGORTGT	RAESNLSSKQLSSDKEQNGVQDP	RHERVVTISGNGSIHS	60
Db	1	MLLGLLLTSALAGORTGT	RAESNLSSKQLSSDKEQNGVQDP	RHERVVTISGNGSIHS	60
Qy	61	PKFPHYPRNMVLRVAVDENVR	IQTFTDERFGLDEPDDICKYDFVEVEPS	DGVSVL	120
Db	61	PKFPHYPRNMVLRVAVDENVR	IQTFTDERFGLDEPDDICKYDFVEVEPS	DGVSVL	120
Qy	121	GRWCSGTVP	QKTSKGNHIRIRFVSDEYFP	SEPGFCIHYSIMPQVTTTSP	SVLPSS 180
Db	121	GRWCSGTVP	QKTSKGNHIRIRFVSDEYFP	SEPGFCIHYSIMPQVTTTSP	SVLPSS 180
Qy	181	LSLDLNNAVTAFSTLEELIRY	LEPDRQVLDLSLYKPTWQLLGKAF	LYGKSKVYNLNL	240

Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 2

US-09-818-943-2  
; Sequence 2, Application US/09818943  
; Patent No. US20020049987A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: LI, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: AASE, Karin  
; APPLICANT: LI, Hong  
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 1064/48487  
; CURRENT APPLICATION NUMBER: US/09/818,943  
; CURRENT FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,507  
; PRIOR FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.8e-174;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISGNGSIHS 60  
QY 61 PKFPHTYPRNMVLWRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
Db 61 PKFPHTYPRNMVLWRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVDSYEPSPGFCIHYSIIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVDSYEPSPGFCIHYSIIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 3

US-09-852-209A-7  
; Sequence 7, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri

; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OSTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 10; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.8e-174;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISGNGSIHS 60  
Db 1 MLLGLLLTTSALAGQRTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISGNGSIHS 60  
QY 61 PKFPHTYPRNMVLWRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
Db 61 PKFPHTYPRNMVLWRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVDSYEPSPGFCIHYSIIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVDSYEPSPGFCIHYSIIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 4

US-10-139-583-43  
; Sequence 43, Application US/10139583  
; Publication No. US20020177193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10/139,583

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; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-139-583-43

Query Match      100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
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QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGSLV 120
Db 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGSLV 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
QY 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNL 240
Db 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCGLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCGLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHECDVCRCGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHECDVCRCGNAGG 345

RESULT 5
US-10-131-600-7
; Sequence 7, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-131-600-7

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
Db 1 MLLGLLLTSSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGSLV 120
Db 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGSLV 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
QY 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNL 240
Db 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCGLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCGLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHECDVCRCGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHECDVCRCGNAGG 345

RESULT 6
US-10-264-361-4
; Sequence 4, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-264-361-4

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
Db 1 MLLGLLLTSSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGSLV 120
Db 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGSLV 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
QY 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNL 240
Db 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNL 240
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Db 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDSLKYPTWQLLGKAFLYGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQCVPRK 300  
QY 301 VTKKYHEVLQRLPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRLPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345

RESULT 7  
US-09-823-033-2  
; Sequence 2, Application US/09823033  
; Patent No. US2002004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G. PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 90.2%; Score 1667; DB 9; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISNGSIHS 60  
Db 1 MSFGLLLTSALAGORQGTQAESNLSSKQFQSNKEQNGVQDQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPPTYPRNTVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDSLKYPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPERWQJLDLEDYRPTWQLLGKAFVFGKSRVVDNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQCVPRK 300  
QY 301 VTKKYHEVLQRLPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 8  
US-09-923-995-4  
; Sequence 4, Application US/09923995  
; Patent No. US20020081700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1  
; FILE REFERENCE: 00-47  
; CURRENT APPLICATION NUMBER: US/09/923,995  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: US 60/223,164  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-995-4

Query Match 90.2%; Score 1667; DB 9; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISNGSIHS 60  
Db 1 MSFGLLLTSALAGORQGTQAESNLSSKQFQSNKEQNGVQDQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPPTYPRNTVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDSLKYPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPERWQJLDLEDYRPTWQLLGKAFVFGKSRVVDNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQCVPRK 300  
QY 301 VTKKYHEVLQRLPKTGKGLHKS LTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG 345

RESULT 9  
US-09-795-006A-149  
; Sequence 149, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 149  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-795-006A-149

Query Match 90.2%; Score 1667; DB 10; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISNGSIHS 60  
Db 1 MSFGLLLTSALAGORQGTQAESNLSSKQFQSNKEQNGVQDQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPPTYPRNTVLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180

Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFSPSEGGCIHYNIVMPQFTBAVSFVLPPSA 180  
QY 181 LSLIDLLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYKKSKVNLNL 240  
Db 181 LSLIDLLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYKKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFVSREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFVSREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
QY 301 VTKKHEVLQLRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQLRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345

RESULT 10  
US-09-978-295A-488  
; Sequence 488, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottsden, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918595  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR FILING DATE: 1998-03-20  
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; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
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; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22



;; PRIOR APPLICATION NUMBER: 60/082700  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083554  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
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;; PRIOR FILING DATE: 1998-05-13  
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;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 10; Length 345;

Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
  
QY 1 MLLGLLLTSLAGORTGTAESSLSKQLSSDKXQGVQDPRHVVVTISNGSIHS 60  
DB 1 MSLFGLLLTSLAGORQGTAESSLSKQFQPSNKEQGVQDQHERIITVTNGSIHS 60  
  
QY 61 PKFPHTYPRNMVLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPDSGVL 120  
DB 61 PREPHTYPRNTVLVRLVAVENVMQLTFDERFGLDEPDDICKYDFVEVEPDSGTL 120  
  
QY 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDEYPPSPGFCIHYSIIMPQVTTTSSVLPPSS 180  
DB 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDEYPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180  
  
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAPLYGKSKVNLNL 240  
DB 181 LPLDLNNAITAFSTLELLIRYLEPDRMQVLDLSLYKPTWQLLGKAPLYGKSKVNDNL 240  
  
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCQVPRK 300  
DB 241 LTEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCQVPSK 300  
  
QY 301 VTKKYHEVLQRPKTGVKGLHKSLLTDVALEHHEEDCVCRNAGG 345  
DB 301 VTKKYHEVLQRPKTGVRLHLSLLTDVALEHHEEDCVCRGSTGG 345

RESULT 11

US-09-978-697-488  
; Sequence 488, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13

1	PRIOR FILING DATE: 1998-04-15	
2	PRIOR APPLICATION NUMBER: 60/081952	
3	PRIOR FILING DATE: 1998-04-15	
4	PRIOR APPLICATION NUMBER: 60/081838	
5	PRIOR FILING DATE: 1998-04-15	
6	PRIOR APPLICATION NUMBER: 60/082568	
7	PRIOR FILING DATE: 1998-04-21	
8	PRIOR APPLICATION NUMBER: 60/082569	
9	PRIOR FILING DATE: 1998-04-21	
10	PRIOR APPLICATION NUMBER: 60/082704	
11	PRIOR FILING DATE: 1998-04-22	
12	PRIOR APPLICATION NUMBER: 60/082804	
13	PRIOR FILING DATE: 1998-04-22	
14	PRIOR APPLICATION NUMBER: 60/082700	
15	PRIOR FILING DATE: 1998-04-22	
16	PRIOR APPLICATION NUMBER: 60/082797	
17	PRIOR FILING DATE: 1998-04-22	
18	PRIOR APPLICATION NUMBER: 60/082796	
19	PRIOR FILING DATE: 1998-04-23	
20	PRIOR APPLICATION NUMBER: 60/083336	
21	PRIOR FILING DATE: 1998-04-27	
22	PRIOR APPLICATION NUMBER: 60/083322	
23	PRIOR FILING DATE: 1998-04-28	
24	PRIOR APPLICATION NUMBER: 60/083392	
25	PRIOR FILING DATE: 1998-04-29	
26	PRIOR APPLICATION NUMBER: 60/083495	
27	PRIOR FILING DATE: 1998-04-29	
28	PRIOR APPLICATION NUMBER: 60/083496	
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34	PRIOR APPLICATION NUMBER: 60/083554	
35	PRIOR FILING DATE: 1998-04-29	
36	PRIOR APPLICATION NUMBER: 60/083558	
37	PRIOR FILING DATE: 1998-04-29	
38	PRIOR APPLICATION NUMBER: 60/083559	
39	PRIOR FILING DATE: 1998-04-29	
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41	PRIOR FILING DATE: 1998-04-29	
42	PRIOR APPLICATION NUMBER: 60/083742	
43	PRIOR FILING DATE: 1998-04-30	
44	PRIOR APPLICATION NUMBER: 60/084366	
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53	PRIOR FILING DATE: 1998-05-07	
54	PRIOR APPLICATION NUMBER: 60/084640	
55	PRIOR FILING DATE: 1998-05-07	
56	PRIOR APPLICATION NUMBER: 60/084598	
57	PRIOR FILING DATE: 1998-05-07	
58	PRIOR APPLICATION NUMBER: 60/084600	
59	PRIOR FILING DATE: 1998-5-07	
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61	PRIOR FILING DATE: 1998-05-07	
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63	PRIOR FILING DATE: 1998-05-07	
64	PRIOR APPLICATION NUMBER: 60/085339	
65	PRIOR FILING DATE: 1998-05-13	
66	PRIOR APPLICATION NUMBER: 60/085338	
67	PRIOR FILING DATE: 1998-05-13	
68	PRIOR APPLICATION NUMBER: 60/085323	
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70	PRIOR APPLICATION NUMBER: 60/085582	
71	PRIOR FILING DATE: 1998-05-15	
72	PRIOR APPLICATION NUMBER: 60/085700	
73	PRIOR FILING DATE: 1998-05-15	

;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 10; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGRTGTRAESNLSSKQLSSDKQNGVQDPHRRVVTISNGSGSIHS 60  
DB 1 MSLFLGLLLTSLALAGRTGTRAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60  
QY 61 PKFPHYPRNMYLVRLVAVDENVRIOQLTDFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120  
DB 61 PRFPHYPRNMYLVRLVAVDENVRIOQLTDFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCSGTVPKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLNNVAFSTLEELIRVLEDRWQVDLSLYKPTWQLLGAFLYGGKSKVNNL 240  
DB 181 LPLDLNNVAFSTLEELIRVLEDRWQVDLSLYKPTWQLLGAFLYGGKSKVNNL 240  
QY 241 LKEEYKLSCTPRNFSVSIRELKRDTTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
DB 241 LKEEYKLSCTPRNFSVSIRELKRDTTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300  
QY 301 VTKYHEVLQRPKTVGKGLHLSLTDVALEHHEEDCVCVRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHLSLTDVALEHHEEDCVCVRGNAGG 345

## RESULT 12

US-09-978-192A-488  
; Sequence 488, Application US/09978192A  
; Patent No. US20020177553A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas P.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630PLC9  
;; CURRENT APPLICATION NUMBER: US/09/978,192A  
;; CURRENT FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: 60/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/064249  
;; PRIOR FILING DATE: 1997-11-03  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066364  
;; PRIOR FILING DATE: 1997-11-21  
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Qy 121 GRWCGSVTPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSVTPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNVMPQFTEAVSPSVLPSSA 180  
  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPRMOVDLSLYKPTWQLLKGKFLYKSKSVNLLN 240  
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Qy 241 LKEEVLKXCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPK 300  
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; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC63  
CURRENT FILING DATE: 2001-10-24  
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PRIOR FILING DATE: 2001-10-24  
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PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-05-06

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APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC7  
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CURRENT FILING DATE: 2001-10-15  
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Db 301 VTKKYHEVLQLRPKTKGVLGKLSLTDVALEHHEBCDVCVRGSTGG 345

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Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi

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/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
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/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
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/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match          90.2%; Score 1667; DB 11; Length 345;
Best Local Similarity 87.0%; Pred. No. 4.5e-156;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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Db 1 MSLFGLLLITLSALAGORQGTQAESNLSSKQFSSNKQNGVQDPQHERITVTSTNGSIHS 60
QY 61 PKFPHYPRNMVWLVRVLVAVDENVRITQLTDFERFGLDEPDDICKYDFVEVEPSDGSVL 120
Db 61 PRFPHYPRNTVLVWRLVAVENVRITQLTDFERFGLDEPDDICKYDFVEVEPSDGTIL 120
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPQFCIHYSIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPGKQISKGQIRIRFVSDVEYFPSEPQFCIHYNIVMPQFTEAVSPSVLPSSA 180
QY 181 LSLDLLNNAVTAFTLEELIRYLEPRDQVOLDLSYKPTWQLLKGAFLYGKSKVNNLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWOLDLELYRPTWQLLKGAFVFGKSRVVDLNL 240
QY 241 LKEEVKLYSCYPRNFSVSIREELKTDITFWPGCLLVKRCGCGNACCLHNCNCCVPRK 300
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Db 241 LEEVRLYSLCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

Qy 301 VTKYHEVLQRLPKTGVKGLHKSITDVALEHHECDVCVRGNAGG 345  
Db 301 VTKYHEVLQRLPKTGVKGLHKSITDVALEHHECDVCVRGNAGG 345

RESULT 15

US-09-796-753-6  
; Sequence 6, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796,753  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/183,175  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 09/223,094  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/223,546  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/224,246  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/259,388  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/122,458  
; PRIOR FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 09/312,359  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/336,536  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 09/342,687  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 09/345,464  
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; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 09/399,723  
; PRIOR FILING DATE: 1999-09-20  
; PRIOR APPLICATION NUMBER: 09/409,634  
; PRIOR FILING DATE: 1999-09-30  
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; PRIOR FILING DATE: 2000-02-25  
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; PRIOR APPLICATION NUMBER: 09/572,002  
; PRIOR FILING DATE: 2000-05-14  
; PRIOR APPLICATION NUMBER: 09/597,993  
; PRIOR FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/599,596  
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; PRIOR APPLICATION NUMBER: 09/630,334  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: 09/606,565  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/606,317  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/665,666  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 09/677,751  
; PRIOR FILING DATE: 2000-09-30  
; NUMBER OF SEQ ID NOS: 162  
; SEQ ID NO 6  
; LENGTH: 345  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-796-753-6

Query Match 90.2%; Score 1667; DB 11; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTITSGNSIHS 60  
Db 1 MSLFGLLLLSALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTITSGNSIHS 60  
Qy 61 PKPHTYPRNMVILVWRLVANDENVRIQLTFDERFGLGLEDPEDDICKYDFVEVEEPESDGVL 120  
Db 61 PRFPHTYPRNTVLVWRLVAVENVVMIQLTFDERFGLGLEDPEDDICKYDFVEVEEPESDGVL 120  
Qy 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDRYFFSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDRYFFSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Qy 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLLQKAFLYGKSKVNNLML 240  
Db 181 LPLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWQLLQKAFLYGKSKVNNLML 240  
Qy 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300  
Qy 301 VTKYHEVLQRLPKTGVKGLHKSITDVALEHHECDVCVRGNAGG 345  
Db 301 VTKYHEVLQRLPKTGVKGLHKSITDVALEHHECDVCVRGNAGG 345

Search completed: November 25, 2003, 21:17:06  
Job time : 25.3006 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:19 ; Search time 169.42 Seconds  
(without alignments)  
1852.926 Million cell updates/sec

Title: US-09-852-209A-7

Perfect score: 1848

Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHBECDVCGRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA Main:\*

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2: /cgn2\_6/ptodata/1/paa/US07 COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1848	100.0	345	17	US-09-304-216-35	Sequence 35, Appl
3	1848	100.0	345	18	US-09-410-349A-7	Sequence 7, Appl
4	1848	100.0	345	19	US-09-540-703-4	Sequence 4, Appl
5	1848	100.0	345	19	US-09-541-752-43	Sequence 43, Appl
6	1848	100.0	345	20	US-09-695-121-4	Sequence 43, Appl
7	1848	100.0	345	21	US-09-706-968-43	Sequence 43, Appl
8	1848	100.0	345	23	US-09-818-943-2	Sequence 2, Appl
9	1848	100.0	345	23	US-09-823-033-4	Sequence 4, Appl
10	1848	100.0	345	23	US-09-852-209-7	Sequence 7, Appl
11	1848	100.0	345	23	US-09-852-209A-7	Sequence 7, Appl
12	1848	100.0	345	27	US-10-131-600-7	Sequence 7, Appl
13	1848	100.0	345	27	US-10-139-583-43	Sequence 43, Appl
14	1848	100.0	345	28	US-10-264-361-4	Sequence 4, Appl
15	1848	100.0	345	29	US-10-303-997B-7	Sequence 7, Appl
16	1667	90.2	345	1	PCT-US01-43523-286	Sequence 286, App
17	1667	90.2	345	1	PCT-US02-24563-286	Sequence 286, App
18	1667	90.2	345	1	PCT-US03-04213-34	Sequence 34, Appl
19	1667	90.2	345	1	PCT-US99-01574-2	Sequence 2, Appl
20	1667	90.2	345	1	PCT-US99-15783-4	Sequence 4, Appl
21	1667	90.2	345	1	PCT-US99-31025-2	Sequence 2, Appl
22	1667	90.2	345	15	US-09-184-216-2	Sequence 2, Appl
23	1667	90.2	345	16	US-09-207-120-2	Sequence 2, Appl
24	1667	90.2	345	16	US-09-223-546-2	Sequence 2, Appl
25	1667	90.2	345	16	US-09-237-705-2	Sequence 2, Appl
26	1667	90.2	345	16	US-09-267-213-2	Sequence 2, Appl
27	1667	90.2	345	17	US-09-304-216-33	Sequence 33, Appl
28	1667	90.2	345	17	US-09-380-138-488	Sequence 488, App
29	1667	90.2	345	18	US-09-458-690A-4	Sequence 4, Appl
30	1667	90.2	345	18	US-09-471-179-2	Sequence 2, Appl
31	1667	90.2	345	19	US-09-540-703-2	Sequence 2, Appl
32	1667	90.2	345	19	US-09-541-752-2	Sequence 2, Appl
33	1667	90.2	345	19	US-09-599-596-2	Sequence 2, Appl
34	1667	90.2	345	20	US-09-662-783-24	Sequence 24, Appl
35	1667	90.2	345	20	US-09-685-330-24	Sequence 24, Appl
36	1667	90.2	345	20	US-09-688-312-51	Sequence 51, Appl
37	1667	90.2	345	20	US-09-695-121-2	Sequence 2, Appl
38	1667	90.2	345	21	US-09-706-968-2	Sequence 2, Appl
39	1667	90.2	345	21	US-09-723-749-2	Sequence 2, Appl
40	1667	90.2	345	22	US-09-795-006A-149	Sequence 149, App
41	1667	90.2	345	22	US-09-796-753-6	Sequence 6, Appl
42	1667	90.2	345	23	US-09-823-033-2	Sequence 2, Appl
43	1667	90.2	345	24	US-09-918-585A-488	Sequence 488, App
44	1667	90.2	345	24	US-09-923-995-4	Sequence 4, Appl
45	1667	90.2	345	24	US-09-929-404-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US99-22668-7  
; Sequence 7, Application PC/TUS9922668B  
; GENERAL INFORMATION:  
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER  
; CURRENT APPLICATION NUMBER: PCT/US99/22668B  
; CURRENT FILING DATE: 1999-09-30  
; EARLIER APPLICATION NUMBER: 60/102,461  
; EARLIER FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/108,109  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 60/110,749  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 60/113,002  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 60/135,426  
; EARLIER FILING DATE: 1999-05-21  
; EARLIER APPLICATION NUMBER: 60/144,022  
; EARLIER FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39

DNA CODING

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 345

TYPE: PRT

ORGANISM: Murinae gen. sp.

CT-US99-22668-7

Query Match 100.0%; Score 1848; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2b 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
QY 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
Db 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCGSTVPGKQTSKGNHIRIRFVSDYFPPSGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRIRFVSDYFPPSGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
Db 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 2

US-09-304-216-35  
; Sequence 35, Application US/09304216  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19X  
; CURRENT FILING DATE: 1999-05-03  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-09-304-216-35

Query Match 100.0%; Score 1848; DB 17; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
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Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 3

US-09-410-349A-7  
; Sequence 7, Application US/09410349A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: FONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/410,349A  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.

US-09-410-349A-7

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Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
Db 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
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Db 121 GRWCGSTVPGKQTSKGNHIRIRFVSDYFPPSGFCIHYSIIMPQVTTTSPSVLPSS 180  
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Db 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
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Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
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Db 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 4

US-09-540-703-4

; Sequence 4, Application US/09540703  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12X  
; CURRENT APPLICATION NUMBER: US/09/540,703  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-540-703-4

Query Match 100.0%; Score 1848; DB 19; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPSDGSVL 120  
DB 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
DB 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 5

US-09-541-752-43

; Sequence 43, Application US/09541752  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/541,752  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-541-752-43

Query Match 100.0%; Score 1848; DB 19; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPSDGSVL 120  
DB 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
DB 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 6

US-09-695-121-4

; Sequence 4, Application US/09695121  
; GENERAL INFORMATION:  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS  
; FILE REFERENCE: 00-53  
; CURRENT APPLICATION NUMBER: US/09/695,121  
; CURRENT FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-695-121-4

Query Match 100.0%; Score 1848; DB 20; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPSDGSVL 120  
DB 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
DB 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCCQVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 2  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Murinae gen. sp.  
 US-09-818-943-2

Query Match 100.0%; Score 1848; DB 23; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISNGSIHS 60  
 DB 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISNGSIHS 60

QY 61 PKFPHYPRNMVLVRLVAVDENVRILQITFDRFGLDEPDDICKYDFVEVEEPPSGSVL 120  
 DB 61 PKFPHYPRNMVLVRLVAVDENVRILQITFDRFGLDEPDDICKYDFVEVEEPPSGSVL 120

QY 121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPSS 180  
 DB 121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPSS 180

QY 181 LSLDLNNAVTAFSTLEELIRYLDPDRQVLDLSLYKFTWLLGKAFLYGKSKVNLNL 240  
 DB 181 LSLDLNNAVTAFSTLEELIRYLDPDRQVLDLSLYKFTWLLGKAFLYGKSKVNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

QY 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345  
 DB 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 9  
 US-09-823-033-4  
 Sequence 4, Application US/09823033  
 GENERAL INFORMATION:  
 APPLICANT: Gilbertson, Debra G.  
 APPLICANT: Hart, Charles E.  
 TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
 TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
 FILE REFERENCE: 00-12  
 CURRENT APPLICATION NUMBER: US/09/823,033  
 CURRENT FILING DATE: 2001-03-29  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 4  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-09-823-033-4

Query Match 100.0%; Score 1848; DB 23; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISNGSIHS 60  
 DB 1 MLLGLLLTSALAGORTGTRAESNLSSKLQSDKEQNGVQDPRHVRVVTISNGSIHS 60

QY 61 PKFPHYPRNMVLVRLVAVDENVRILQITFDRFGLDEPDDICKYDFVEVEEPPSGSVL 120  
 DB 61 PKFPHYPRNMVLVRLVAVDENVRILQITFDRFGLDEPDDICKYDFVEVEEPPSGSVL 120

QY 121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPSS 180  
 DB 121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPVLPSS 180

QY 181 LSLDLNNAVTAFSTLEELIRYLDPDRQVLDLSLYKFTWLLGKAFLYGKSKVNLNL 240  
 DB 181 LSLDLNNAVTAFSTLEELIRYLDPDRQVLDLSLYKFTWLLGKAFLYGKSKVNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300  
 DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

QY 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345  
 DB 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 8  
 US-09-818-943-2  
 Sequence 2, Application US/09818943  
 GENERAL INFORMATION:  
 APPLICANT: ERIKSSON, Ulf  
 APPLICANT: LI, Xuri  
 APPLICANT: PONTEN, Annica  
 APPLICANT: AASE, Karin  
 APPLICANT: LI, Hong  
 TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F  
 FILE REFERENCE: 1064/4847  
 CURRENT APPLICATION NUMBER: US/09/818,943  
 CURRENT FILING DATE: 2001-03-28  
 PRIOR APPLICATION NUMBER: US 60/192,507  
 PRIOR FILING DATE: 2000-03-28

```
Db 181 LSLDLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Qy 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345
Db 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345

RESULT 10
US-09-852-209-7
; Sequence 7, Application US/09852209
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRN
; ORGANISM: Murinae gen. sp.
US-09-852-209-7

Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTSAAGORTGTGAESNLSSKQLQSSDKEQNGVQDPRHVRVTISGNGSIHS 60
Db 1 MLLGLLLLTSAAGORTGTGAESNLSSKQLQSSDKEQNGVQDPRHVRVTISGNGSIHS 60
Qy 61 PKFPHYPRNMVWLVRVAVDENVRVQLTDFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVWLVRVAVDENVRVQLTDFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Db 181 LSLDLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Qy 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345
Db 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345

RESULT 12
US-10-131-600-7
; Sequence 7, Application US/10131600
; GENERAL INFORMATION:
```

```
Db 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345
Qy 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345

RESULT 11
US-09-852-209A-7
; Sequence 7, Application US/09852209A
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRN
; ORGANISM: Murinae gen. sp.
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTSAAGORTGTGAESNLSSKQLQSSDKEQNGVQDPRHVRVTISGNGSIHS 60
Db 1 MLLGLLLLTSAAGORTGTGAESNLSSKQLQSSDKEQNGVQDPRHVRVTISGNGSIHS 60
Qy 61 PKFPHYPRNMVWLVRVAVDENVRVQLTDFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVWLVRVAVDENVRVQLTDFDRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Db 181 LSLDLNNAVAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRK 300
Qy 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345
Db 301 VTKKYHEVLQRPKTGVKGLHLSLTDVALEHHEEDCVCVRGNAGG 345

RESULT 12
US-10-131-600-7
; Sequence 7, Application US/10131600
; GENERAL INFORMATION:
```

APPLICANT: ERIKSSON, Ulf  
 APPLICANT: AASE, Karin  
 APPLICANT: LEE, Xuri  
 APPLICANT: PONTEN, Annica  
 APPLICANT: UUTELA, Marko  
 APPLICANT: ALITALO, Kari  
 APPLICANT: OESTMAN, Arne  
 APPLICANT: HELDIN, Carl-Henrik  
 APPLICANT: BETHSOLTZ, Christer  
 TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
 TITLE OF INVENTION: THEREOF, AND USES THEREOF  
 FILE REFERENCE: 08-410349-Eriksson et al-1064-44740  
 CURRENT APPLICATION NUMBER: US/10/131,600  
 PRIOR FILING DATE: 2002-04-25  
 RIOR APPLICATION NUMBER: US/09/410,349  
 RIOR FILING DATE: 1999-09-30  
 RIOR APPLICATION NUMBER: 60/108,109  
 RIOR FILING DATE: 1998-11-12  
 RIOR APPLICATION NUMBER: 60/110,749  
 RIOR FILING DATE: 1998-12-03  
 RIOR APPLICATION NUMBER: 60/113,002  
 RIOR FILING DATE: 1998-12-18  
 RIOR APPLICATION NUMBER: 60/135,426  
 RIOR FILING DATE: 1999-05-21  
 RIOR APPLICATION NUMBER: 60/144,022  
 RIOR FILING DATE: 1999-07-15  
 NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 7  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Murinae gen. sp.  
 -10-131-600-7

Query Match 100.0%; Score 1848; DB 27; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 / 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISGNSIHS 60  
 b 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISGNSIHS 60  
 y 61 PKFPHYPRNNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 b 61 PKFPHYPRNNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 y 121 GRWCGGTVPCKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPOVTETTSPLVPPSS 180  
 b 121 GRWCGGTVPCKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPOVTETTSPLVPPSS 180  
 y 181 LSLLDNNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
 b 181 LSLLDNNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
 y 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 b 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 y 301 VTKKHEVLQRLPRTGKGLHKSITDVALEHHEEDCVCRCGNAGG 345  
 b 301 VTKKHEVLQRLPRTGKGLHKSITDVALEHHEEDCVCRCGNAGG 345

RESULT 13  
 US-10-139-583-43  
 ; Sequence 43, Application US/10139583  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gao, Zeren  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Piddington, Chrl O.  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Shoemaker, Kimberly E.  
 ; APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.  
 TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVSCF3  
 FILE REFERENCE: 98-60  
 CURRENT APPLICATION NUMBER: US/10/139,583  
 PRIOR FILING DATE: 2002-05-02  
 PRIOR APPLICATION NUMBER: 09/457,066  
 PRIOR FILING DATE: 1999-12-07  
 NUMBER OF SEQ ID NOS: 50  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 43  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-139-583-43

Query Match 100.0%; Score 1848; DB 27; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISGNSIHS 60  
 Db 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISGNSIHS 60  
 Qy 61 PKFPHYPRNNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 Db 61 PKFPHYPRNNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 Qy 121 GRWCGGTVPCKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPOVTETTSPLVPPSS 180  
 Db 121 GRWCGGTVPCKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPOVTETTSPLVPPSS 180  
 Qy 181 LSLLDNNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
 Db 181 LSLLDNNNAVTAFSTLEELIRYLEPDRQVQDLSLYKPTWQLLKAFLYGKSKVNNL 240  
 Qy 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 Qy 301 VTKKHEVLQRLPRTGKGLHKSITDVALEHHEEDCVCRCGNAGG 345  
 Db 301 VTKKHEVLQRLPRTGKGLHKSITDVALEHHEEDCVCRCGNAGG 345

RESULT 14  
 US-10-264-361-4  
 ; Sequence 4, Application US/10264361  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbertson, Debra G.  
 ; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS  
 ; FILE REFERENCE: 00-53  
 ; CURRENT APPLICATION NUMBER: US/10/264,361  
 ; CURRENT FILING DATE: 2002-10-03  
 ; PRIOR APPLICATION NUMBER: US/09/695,121  
 ; PRIOR FILING DATE: 2000-10-23  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-264-361-4

Query Match 100.0%; Score 1848; DB 28; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISGNSIHS 60  
 Db 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISGNSIHS 60  
 Qy 61 PKFPHYPRNNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120



Db 61 PKPHTYPRNMVLRVAVDENVRIOQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEBLIRYLEPRWQVDLDSLYKPTWQLLGKAFLYGKSKVYNLNL 240  
Db 181 LSLDLNNAVTAFSTLEBLIRYLEPRWQVDLDSLYKPTWQLLGKAFLYGKSKVYNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 15  
US-10-303-997B-7  
; Sequence 7, Application US/10303997B  
; GENERAL INFORMATION:  
; APPLICANT: LI, Xuri  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: CARMELIET, Peter  
; APPLICANT: COLLUM, Desire  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN  
; FILE REFERENCE: 029065.44740C3  
; CURRENT APPLICATION NUMBER: US/10/303,997B  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: US 60/102,461  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: US 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: US 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-10-303-997B-7

Query Match 100.0%; Score 1848; DB 29; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISNGSIHS 60  
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISNGSIHS 60  
QY 61 PKPHTYPRNMVLRVAVDENVRIOQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120  
Db 61 PKPHTYPRNMVLRVAVDENVRIOQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEBLIRYLEPRWQVDLDSLYKPTWQLLGKAFLYGKSKVYNLNL 240  
Db 181 LSLDLNNAVTAFSTLEBLIRYLEPRWQVDLDSLYKPTWQLLGKAFLYGKSKVYNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300  
QY 301 VTKKYHEVLQLRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

Search completed: November 25, 2003, 21:14:50  
Job time : 170.753 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:59 ; Search time 13.6905 Seconds  
(without alignments)  
1293.384 Million cell updates/sec

Title: US-09-852-209A-7  
Perfect score: 1848  
Sequence: 1 MLLGLLLTTSALAGQRTGT.....DVALEHHEEDCVCRGNAGG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 271250 seqs, 51324744 residues

Total number of hits satisfying chosen parameters: 271250

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New.\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pcp.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1848	100.0	345	5	US-09-457-066-43
2	1848	100.0	345	5	US-09-876-813-35
3	1667	90.2	345	1	PCT-US03-26491-191
4	1667	90.2	345	5	US-09-457-066-2
5	1667	90.2	345	5	US-09-876-813-33
6	1667	90.2	345	6	US-10-648-593-191
7	1667	90.2	345	6	US-10-471-221-1
8	1667	90.2	345	7	US-60-487-610-1644
9	1667	90.2	345	7	US-60-485-450-1042
10	1659	89.8	345	5	US-09-830-320A-4
11	1267.5	68.6	282	6	US-10-471-221-5
12	1204.5	65.2	302	5	US-09-876-813-57
13	1200	64.9	303	5	US-09-876-813-54
14	1077.5	58.3	305	1	PCT-US00-28803-7
15	1035.5	56.0	317	5	US-09-876-813-56
16	1019	55.1	316	5	US-09-876-813-55
17	752	40.7	370	5	US-09-457-066-37
18	752	40.7	370	5	US-09-876-813-2
19	752	40.7	370	6	US-10-321-962-4
20	752	40.7	370	6	US-10-606-055-2
21	746.5	40.4	370	5	US-09-876-813-53
22	746.5	40.4	370	6	US-10-321-962-8
23	746.5	40.4	370	6	US-10-606-055-4
24	720	39.0	167	6	US-10-471-221-6
25	549	29.7	111	6	US-10-471-221-2
26	440.5	23.8	261	6	US-10-321-962-10

RESULT 1  
US-09-457-066-43  
; Sequence 43, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-457-066-43

ALIGNMENTS

27	324.5	17.6	132	6	US-10-321-962-6	Sequence 6, Appli
28	312.5	16.9	154	6	US-10-321-962-12	Sequence 12, Appl
29	191	10.3	110	6	US-10-321-962-14	Sequence 14, Appl
30	190	10.3	823	7	US-60-495-114-2259	Sequence 2259, Ap
31	190	10.3	823	7	US-60-495-114-2266	Sequence 2266, Ap
32	190	10.3	823	7	US-60-495-114-2267	Sequence 2267, Ap
33	188	10.2	726	7	US-60-495-114-2251	Sequence 2251, Ap
34	185	10.0	1015	7	US-60-495-114-1841	Sequence 1841, Ap
35	183.5	9.9	730	5	US-09-830-320A-12	Sequence 12, Appl
36	183.5	9.9	730	7	US-60-495-114-2257	Sequence 2257, Ap
37	183.5	9.9	730	7	US-60-495-114-2260	Sequence 2260, Ap
38	183.5	9.9	730	7	US-60-495-114-2268	Sequence 2268, Ap
39	181	9.8	466	7	US-60-495-114-2262	Sequence 2262, Ap
40	181	9.8	717	7	US-60-495-114-2252	Sequence 2252, Ap
41	181	9.8	717	7	US-60-495-114-2253	Sequence 2253, Ap
42	181	9.8	717	7	US-60-495-114-2253	Sequence 2263, Ap
43	181	9.8	986	6	US-10-474-794-242	Sequence 242, App
44	181	9.8	986	7	US-60-495-114-2254	Sequence 2254, Ap
45	181	9.8	986	7	US-60-495-114-2264	Sequence 2264, Ap

Query Match	100.0%;	Score 1848;	DB 5;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 3.3e-152;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLLGLLLTTSALAGQRTGTGTRAESNLSSKLQSSDKEQNGVDPHRRVVTISGNSIHS	60	
Db	1	MLLGLLLTTSALAGQRTGTGTRAESNLSSKLQSSDKEQNGVDPHRRVVTISGNSIHS	60	
QY	61	PKFPHTYPNMYLWRLVAVDENVRQLTFDRFGLDEPDDICKYDFVEVEPSPDGSVL	120	
Db	61	PKFPHTYPNMYLWRLVAVDENVRQLTFDRFGLDEPDDICKYDFVEVEPSPDGSVL	120	
QY	121	GRWCSTGTPGKQTSKGNHIRFRFVSDYFPSPGFCIHYSIMPOVTETTSVLPSS	180	
Db	121	GRWCSTGTPGKQTSKGNHIRFRFVSDYFPSPGFCIHYSIMPOVTETTSVLPSS	180	
QY	181	LSLDLNNAVTAFSTLEELIRYLEPDRQVDDLSLYKPTWQLLGKFLYKSKVNNLNL	240	
Db	181	LSLDLNNAVTAFSTLEELIRYLEPDRQVDDLSLYKPTWQLLGKFLYKSKVNNLNL	240	
QY	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWFGCLLVKRCGNCACCLHNCNCCQVPRK	300	
Db	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWFGCLLVKRCGNCACCLHNCNCCQVPRK	300	
QY	301	VTKKHEVQLPQKTVGKGLHSLTDVALEHHEBCDVCRCNAGG	345	

Db 301 VTXYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 2  
US-09-876-813-35  
; Sequence 35, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US/09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US/60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US/60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-876-813-35

Query Match 100.0%; Score 1848; DB 5; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.3e-152;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNSIHS 60  
DB 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNSIHS 60  
QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120  
DB 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120  
QY 121 GRWCGSTVPKGKTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCGSTVPKGKTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240  
DB 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTXYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTXYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 3  
PCT-US03-26491-191  
; Sequence 191, Application PC/TUS0326491  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT  
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/26491  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 191  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-26491-191

Query Match 90.2%; Score 1667; DB 1; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNSIHS 60  
DB 1 MSLFGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNSIHS 60  
QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120  
DB 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120  
QY 121 GRWCGSTVPKGKTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCGSTVPKGKTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSIDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240  
DB 181 LPLDLLNNAITAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTXYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTXYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 4  
US-09-457-066-2  
; Sequence 2, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-457-066-2

Query Match 90.2%; Score 1667; DB 5; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNSIHS 60  
DB 1 MSLFGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNSIHS 60  
QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120  
DB 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120  
QY 121 GRWCGSTVPKGKTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCGSTVPKGKTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180

Db 121 GRWCGSTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTAVSPSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPRQVQDLSLYKPTWQLLQKAFYLGKSKVNNLNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPRQVQDLSLYKPTWQLLQKAFYLGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVIRELKRKTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVIRELKRKTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 5

US-09-876-813-33  
; Sequence 33, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US/09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US/60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US/60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-876-813-33

Query Match 90.2%; Score 1667; DB 5; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHVRVVTISGNGSIHS 60  
Db 1 MSLFGLLLLTALAGORQGTQAESNLSSKQFQSSNKQNGVODPQHERIITVSTNGSIHS 60  
QY 61 PKFPHYPRNVMVLVWRLVAVDENVRIOITFDRFGLGDEPDDICKYDFVEVEEPSDGSVL 120  
Db 61 PRFPHYPRNTVLVWRLVAVBENVWVQITFDRFGLGDEPDDICKYDFVEVEEPSDGTIL 120  
QY 121 GRWCGSTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTAVSPSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPRQVQDLSLYKPTWQLLQKAFYLGKSKVNNLNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPRQVQDLSLYKPTWQLLQKAFYLGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVIRELKRKTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVIRELKRKTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 6

US-10-648-593-191

; Sequence 191, Application US/10648593  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THE  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 NP  
; CURRENT APPLICATION NUMBER: US/10/648,593  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 191  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-593-191

Query Match 90.2%; Score 1667; DB 6; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHVRVVTISGNGSIHS 60  
Db 1 MSLFGLLLLTALAGORQGTQAESNLSSKQFQSSNKQNGVODPQHERIITVSTNGSIHS 60  
QY 61 PKFPHYPRNVMVLVWRLVAVDENVRIOITFDRFGLGDEPDDICKYDFVEVEEPSDGSVL 120  
Db 61 PRFPHYPRNTVLVWRLVAVBENVWVQITFDRFGLGDEPDDICKYDFVEVEEPSDGTIL 120  
QY 121 GRWCGSTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQISGKQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTAVSPSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPRQVQDLSLYKPTWQLLQKAFYLGKSKVNNLNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPRQVQDLSLYKPTWQLLQKAFYLGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVIRELKRKTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVIRELKRKTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 7

US-10-471-221-1  
; Sequence 1, Application US/10471221  
; GENERAL INFORMATION:  
; APPLICANT: Janssen Pharmaceutica N.V.  
; TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation  
; FILE REFERENCE: JAB 1687  
; CURRENT APPLICATION NUMBER: US/10/471,221  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US/60/274901  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-471-221-1

Query Match 90.2%; Score 1667; DB 6; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHVRVVTISGNGSIHS 60  
Db 1 MSLFGLLLLTALAGORQGTQAESNLSSKQFQSSNKQNGVODPQHERIITVSTNGSIHS 60

Db 1 MSLFGLLLTALSAGORQGTGAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
Qy 61 PKPPTYPRNMVLVWRLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVEPSDGSVL 120  
Db 61 PRPPTYPRNTVLVWRLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVEPSDGTIL 120  
Qy 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTTSPVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDVEYFPSPGFCIHYNVMPQFTEAVSVPSPSA 180  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFVFGKSRVVDLNL 240  
Qy 241 LKEEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LTEEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
Qy 301 VTXXHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345  
Db 301 VTXXHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGSTGG 345

## RESULT 8

US-60-487-610-1644  
; Sequence 1644, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Honglin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1644  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-487-610-1644

Query Match 90.2%; Score 1667; DB 7; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLTALSAGORQGTGAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
Db 1 MSLFGLLLTALSAGORQGTGAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
Qy 61 PKPPTYPRNMVLVWRLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVEPSDGSVL 120  
Db 61 PRPPTYPRNTVLVWRLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVEPSDGTIL 120  
Qy 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTTSPVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDVEYFPSPGFCIHYNVMPQFTEAVSVPSPSA 180  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFVFGKSRVVDLNL 240  
Qy 241 LKEEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LTEEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
Qy 301 VTXXHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345  
Db 301 VTXXHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGSTGG 345

## RESULT 9

US-60-485-450-1042  
; Sequence 1042, Application US/60485450  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: CHANG, Sheng-Yung  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001470  
; CURRENT APPLICATION NUMBER: US/60/485,450  
; CURRENT FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 47859  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1042  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-485-450-1042

Query Match 90.2%; Score 1667; DB 7; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLTALSAGORQGTGAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
Db 1 MSLFGLLLTALSAGORQGTGAESNLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
Qy 61 PKPPTYPRNMVLVWRLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVEPSDGSVL 120  
Db 61 PRPPTYPRNTVLVWRLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVEPSDGTIL 120  
Qy 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDVEYFPSPGFCIHYSIIMPQVTTTSPVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDVEYFPSPGFCIHYNVMPQFTEAVSVPSPSA 180  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFVFGKSRVVDLNL 240  
Qy 241 LKEEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LTEEVLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
Qy 301 VTXXHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345  
Db 301 VTXXHEVLQRLPKTGVKGLHKSITDVALEHHEECDCVCRGSTGG 345

## RESULT 10

US-09-830-320A-4  
; Sequence 4, Application US/09830320A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: GORGLER, Karl J.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: AU-YOUNG, Janice K.  
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES  
; FILE REFERENCE: PF-0627 USN  
; CURRENT APPLICATION NUMBER: US/09/830,320A  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: PCT/US99/25458  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: US 60/183,024  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: US 60/155,216  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/172,233  
; PRIOR FILING DATE: 1999-05-17

```
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No.: 4163378CD1
US-09-830-320A-4

Query Match      89.8%; Score 1659; DB 5; Length 345;
Best Local Similarity 86.7%; Pred. No. 7.6e-136;
Matches 299; Conservative 27; Mismatches 19; Indels 0; Gaps 0;

QY 1 MLLGLLLTALSAGORTQTRAESNLSSKLQSSDKQNGVQDPQHRHVVITSGNGSIHS 60
DB 1 MSLFGLLLTALSAGORQGTQAESNLSSKQFSSNKEQYGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPPTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEDDICKYDFVEVEEPPSDGVL 120
DB 61 PRPPTYPRNTVLVWRLVAVEENVQLTFDERFGLDEDDICKYDFVEVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPVLPPSS 180
DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300
DB 241 LEEVRLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSGG 345

RESULT 11
US-10-471-221-5
; Sequence 5, Application US/10471221
; GENERAL INFORMATION:
; APPLICANT: Janssen Pharmaceutica N.V.
; FILE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
; CURRENT APPLICATION NUMBER: US/10/471,221
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 60/274901
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-471-221-5

Query Match      68.6%; Score 1267.5; DB 6; Length 282;
Best Local Similarity 69.3%; Pred. No. 4.6e-102;
Matches 239; Conservative 26; Mismatches 17; Indels 63; Gaps 1;

QY 1 MLLGLLLTALSAGORTQTRAESNLSSKLQSSDKQNGVQDPQHRHVVITSGNGSIHS 60
DB 1 MSLFGLLLTALSAGORQGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPPTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEDDICKYDFVEVEEPPSDGVL 120
DB 61 PRPPTYPRNTVLVWRLVAVEENVQLTFDERFGLDEDDICKYDFVEVEEPPSDGTL 120
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPVLPPSS 180
DB 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300
DB 241 LEEVRLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVRPK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHEECDCVCRGSGG 345

RESULT 12
US-09-876-813-57
; Sequence 57, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-57

Query Match      65.2%; Score 1204.5; DB 5; Length 303;
Best Local Similarity 71.3%; Pred. No. 1.5e-96;
Matches 216; Conservative 42; Mismatches 40; Indels 5; Gaps 3;

QY 47 ERVVTISNGSIHSPKPHYTPRNMVLVWRLVAVDENVRQLTFDERFGLDEDDICKY 106
DB 2 DETIQKNGYVQSPRFPNSYPRNLLTWRLHS-QENTRIQLVFDNQFGLAEADICRY 60
QY 107 DFVEVEEPPSDGVL--GRWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSI 163
DB 61 DFVEVEDISETTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYSL 120
QY 164 -MPQVTTTSPVLPPSSLSLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTW 222
DB 121 DFQPAASVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTW 180
QY 223 LGKAFLYGKSKVNNLNLKEEVLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 282
DB 181 LGKAFVGRKSRVVDLNLLEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 240
QY 283 NCACCLHNCNECQCVRPKYTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGN 342
DB 241 NCACCLHNCNECQCVRPKYTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGS 300
QY 343 AGG 345
DB 301 TGG 303
```

```
RESULT 13
US-09-876-813-54
; Sequence 54, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-54

Query Match 64.9%; Score 1200; DB 5; Length 302;
Best Local Similarity 72.4%; Pred. No. 3.6e-96;
Matches 215; Conservative 35; Mismatches 43; Indels 4; Gaps 2;

QY 46 HERVVTISGNSIHSKPPHYPRNMLVWRLVAVDENVRIQLTFDERFGLEDPEDDICK 105
DB 1 HERITVSTNGSIHSKPPHYPRNMLVWRLVAVDENVRIQLTFDERFGLEDPEDDICK 60

QY 106 YDFVEVEEPPSDGVLGRWCSTGTPGKQISKGNIHRIKRVSDYFPEPFCIHYSIIMP 165
DB 61 YDFVEVEEPPSDGTLIGRWCSGTPGKQISKGNIHRIKRVSDYFPEPFCIHYNVMP 120

QY 166 QVTETTSVLPSPSSLSLIDLNNAVTAFTSTLEELIRYLEPDRMQVDLDSLYKPTWLLGK 225
DB 121 QTEAVSPSVLPSPSALPLDLNNAVTAFTSTLEELIRYLEPDRMQVDLDSLYKPTWLLGK 180

QY 226 AFLGKSKVNNMLLKEEVKLYSCTPRNFSVSIREELKSTDTIFWPGCLLVKRCGNCA 285
DB 181 AFVFGKSR-VDLDRNDADAKRYSCTPRNVSNIREELKLANVVFPRCLLVQRCGNCG 239

QY 286 CCLHNCNECQVPRKVKYKHEVLQLRP---KTGVKGLHKSITDVALEHHEECDCVC 339
DB 240 CGTVNRSCTCSGKTKYKHEVLQEPFGHIKRRGRKTMALVDIQLDHERCDIC 296

RESULT 14
PCT-US00-28803-7
; Sequence 7, Application PC/TUS0028803
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Donoho, Gregory
; APPLICANT: Nehls, Michael
; APPLICANT: Hilbun, Erin
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
; FILE REFERENCE: LEX-0070-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/28803
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/160,106
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/162,547
; PRIOR FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-28803-7

Query Match 58.3%; Score 1077.5; DB 1; Length 305;
Best Local Similarity 75.7%; Pred. No. 1.5e-85;
Matches 203; Conservative 27; Mismatches 35; Indels 3; Gaps 1;

QY 1 MLLGLLLTTSALAGQRTGTAENSLSKQLSKQKQNGVQDPRHVRVTVISGNSIHS 60
DB 1 MSLFGLLLTTSALAGQRTQAESNLSSKQFQSSNKQNGVQDQPHERRIITVSTNGSIHS 60

QY 61 PKFPHTYPRNMLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPPSDGVL 120
DB 61 PRFPHTYPRNMLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPPSDGTL 120

QY 121 GRWCSGTPGKQISKGNIHRIKRVSDYFPEPFCIHYSIIMPQVTETTSVLPSPSS 180
DB 121 GRWCSGTPGKQISKGNIHRIKRVSDYFPEPFCIHYNVMPQFTEAVSPSVLPSPSA 180

QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMQVDLDSLYKPTWLLGKAFLYGKSKVNNML 240
DB 181 LPLDLNNAVTAFTSTLEELIRYLEPDRMQVDLDSLYKPTWLLGKAFVFGKSRGDNVEK 240

QY 241 ---LKEEVKLYSCTPRNFSVSIREELK 265
DB 241 EKMLATNFVKYLAEGNFFNIIVKLFKK 268

RESULT 15
US-09-876-813-56
; Sequence 56, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-56

Query Match 56.0%; Score 1035.5; DB 5; Length 317;
Best Local Similarity 60.2%; Pred. No. 6.7e-82;
Matches 192; Conservative 47; Mismatches 57; Indels 23; Gaps 6;

QY 47 ERVVTISGNSIHSKPPHYPRNMLVWRLVAVDENVRIQLTFDERFGLEDPEDDICK 106
DB 2 DETIQKNGYVQSPRPNVPRNMLVWRLVAVDENVRIQLTFDERFGLEDPEDDICK 60

QY 107 DFVEVEEPPSDGVL---GRWCSGTPGKQISKGNIHRIKRVSDYFPEPFCIHYSIIMP 163
DB 61 DFVEVEEPPSDGTLIGRWCSGTPGKQISKGNIHRIKRVSDYFPEPFCIHYSIIMP 120
```



```
Qy 164 --MPQVTETT-----SPSVLPSPSSLSLNNNAVTAFTSLEELIRYLEPD 206
Db 121 DFQPAASSETWESVTSSISGVSNPSVTDp-TLADALDKIAEFDTVEDLLKYFNPE 179
Qy 207 RQVVDLSLYKPTWQLGKAFLYGKSKVNLNLLKEEVKLYSCTPRNFSVSIREELKRT 266
Db 180 SWQEDLENNMYLTPRYGRSY-HDRKSKVDNLNLTTEEVRLYSCTPRNFSVSIREELKRT 238
Qy 267 DTIFWPGCLLVKRCGNCACCLHNCNECQVPRKVKYHEVLQRPKTGVKGLHKS LTD 326
Db 239 DTIFWPGCLLVKRCGNCACCLHNCNECQVPSKVKYHEVLQRPKTGVKGLHKS LTD 298
Qy 327 VALEHHEECDCVCRGNAGG 345
Db 299 VALEHHEECDCVCRGSTGG 317
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Search completed: November 25, 2003, 21:15:41  
Job time : 14.6905 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34 ; Search time 14.7173 Seconds  
(without alignments)  
2254.373 Million cell updates/sec

Title: US-09-852-209A-7

Perfect score: 1848

Sequence: 1 MLLGLLLITSALAGRTGT.....DVALEHHERCDVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	754	40.8	370	JC7592	spinal cord-derive
2	753	40.7	370	JC7591	spinal cord-derive
3	191	10.3	707	JC2218	procollagen C-endo
4	190	10.3	823	A58788	procollagen C-endo
5	183.5	9.9	730	BMH1	procollagen C-endo
6	183.5	9.9	927	JQ0948	A5 antigen precurs
7	181	9.8	986	B58788	procollagen C-endo
8	181	9.8	991	I49540	procollagen C-endo
9	174.5	9.4	3623	T09456	procollagen C-endo
10	160	8.7	3623	T08618	intrinsic factor-B
11	158	8.5	449	A55362	procollagen I C-pr
12	153	8.3	1057	A39288	dorsal-ventral pat
13	147.5	8.0	1524	T30337	polyprotein - Afri
14	145.5	7.9	686	A59271	Ra-reactive factor
15	144	7.8	699	I54763	Ra-reactive factor
16	143.5	7.8	597	S71352	metalloproteinase
17	141.5	7.7	1070	T31069	colloid-BMP-1 like
18	140.5	7.6	3871	T22812	hypothetical prote
19	139	7.5	1594	C1HURB	hensin - rabbit
20	137.5	7.4	705	C1HURB	complement subcomp
21	135.5	7.3	1464	S58984	development protei
22	133.5	7.2	402	JH0403	procollagen I C-pr
23	128	6.9	277	A41735	hyaluronate-bindin
24	127	6.9	419	S69207	vascular endotheli
25	126.5	6.8	579	JC7629	membrane-type friz
26	125.5	6.8	245	1 TVCTSS	platelet-derived g
27	125.5	6.8	767	T30018	hypothetical prote
28	123	6.7	275	JC6506	tumor necrosis fac
29	122.5	6.6	2403	A59386	sanko - human

30	119.5	6.5	2083	2	T42721	CRP-ductin-alpha p
31	117.5	6.4	276	2	A47290	TSG-6 homolog PS4
32	117.5	6.4	1290	2	A57190	ebnerin precursor
33	114.5	6.2	200	2	IS1551	platelet-derived g
34	114.5	6.2	215	2	S08220	platelet-derived g
35	114.5	6.2	226	2	IS1550	platelet-derived g
36	113	6.1	695	1	S05008	complement subcomp
37	112.5	6.1	241	1	PFHUG2	platelet-derived g
38	111.5	6.0	226	1	TMVSS	PDGF-related trans
39	109	5.9	694	2	JC6554	complement subcomp
40	108.5	5.9	148	2	D49530	16k vascular endot
41	107	5.8	321	2	T33161	hypothetical prote
42	104	5.6	319	2	IS1569	UVS.2 protein - Af
43	103.5	5.6	225	2	S25097	platelet-derived g
44	103	5.6	196	2	B28964	platelet-derived g
45	103	5.6	211	1	PFHUG1	platelet-derived g

## ALIGNMENTS

### RESULT 1

JC7592

spinal cord-derived growth factor-B precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001

C;Accession: JC7592

R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280: 733-737, 2001

A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-

A;Reference number: JC7591; MUID:21092670; PMID:11162582

A;Contents: Fetal brain

A;Accession: JC7592

A;Molecule type: mRNA

A;Residues: 1-370 <HAM>

A;Cross-references: DDBJ:AB052170

C;Genetics:

A;Gene: scdgf-B

F;1-17/Domain: secretory signal sequence #status predicted <SIG>

F;18-370/Product: spinal cord-derived growth factor-B #status predicted <SIG>

F;52-170/Region: CUB domain #status predicted

F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr

F;294-308/Region: conserved motif #status predicted

Query Match	40.8%;	Score	754;	DB	2;	Length	370;
Best Local Similarity	46.2%;	Pred. No.	1.4e-55;				
Matches	151;	Conservative	62;	Mismatches	86;	Indels	28;
Gaps	10;						
QY	37	EQNGVQD-PRHERVVTISNGSIHSPKPHPTYPNNMVLVRLVAVDENVRILQTFDERFG	95				
Db	42	ESNHLTDLVRRDENIRVTGTGHVQSPRFPNLSLTLTWRLHS-QBKTRIQLAFDHQFG	100				
QY	96	LEPEDDICKYDFVEVEERSDGS--VLGRWCGSTVFGKOTSGNHRIRFVSDYEPSE	153				
Db	101	LEBAENDICRYDFVEVEDVSESSTVVRGRWCGHKEIPRITSRTNQIKITFQSDDYFAK	160				
QY	154	PGFCIHYSII---MPQ-----VTET-----TSPSVLPFSSSLDLLNNAVTAFT	195				
Db	161	PGFKIYVSFVEDPQPEASINNESVTSFSGVSYHSPSVN-DSTLTADALDKAIAEFT	219				
QY	196	LEELIYLEPDRQVLDLSLYKFTWQLLQKAFYGGKSKVNNLNLLKEFKVLSCTPRNF	255				
Db	220	VEDLLKYFNASQDDLENLMDTPYRGRSY-HERKSK-VLDRLNDVVKRYSCSTRNH	277				
QY	256	SVSIRELKRDTIFWPGCLLVKRCGNCACCLHNCNCCVPRKVTKKYHEVLQLRP--	313				
Db	278	SVNLREELKLTNAVFFPRCLLVQRCGNCGCGTLNWKSCCTSSGKTVKKYHEVLKFEFGH	337				
QY	314	-KTGVKGLKSLTDVALEHHEECDCVC	339				
Db	338	FKERGAKNALVDIQIDHHERCDCIC	364				

```
RESULT 2
JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C:Accession: JC7591
R:Hamada, T.; Uti-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDFP-B, a novel growth factor homologous to SCDFP/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Accession: JC7591
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-references: DDBJ:AB033832
C:Genetics:
A:Gene: scdgp-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor
F:294-308/Region: conserved motif #status predicted
Query Match 40.7%; Score 753; DB 2; Length 370;
Best Local Similarity 45.3%; Pred. No. 1.7e-55;
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;
QY 37 EQNGVQD-PRHERVVTISNGSIHSPKFPHTYPRNMVLVAVDENVRQLTDFERFG 95
DB 42 ESNHLDLYRDETIQVKGNGYQSPFPNSYPRNLLTWLHS-QENTRIQLVFNQFG 100
QY 96 LEDPEDICKYDPVEEESDGSVL--GRWCGSGTVPKGQTSKGNHIRFVSDYFPPSE 153
DB 101 LBEAENDICRYDVEVEDISSETIIRGWCGHKEVPPRIKSRITNQIKITFKSDDYFAK 160
QY 154 PGCIHYSI--MPQVTEI-----SPSVLPSSSLDLNNAVTAFT 195
DB 161 PGKIIYISLLEDQPAASSTNVESTSIISGVSYNSPSTDP-TLIADALDKKIAEFT 219
QY 196 LEEILRYLPDRQVLDLSLYKPTQLLQKAFYLGKSKVYNLLKEEVLYSCTPRNF 255
DB 220 VEDLLKYFNPESQWEDLENLYLTPRYGRSY-HSRKSK-VDLDRNLNDAKRYSCTPRNY 277
QY 256 SVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNCCQVPRKVTYKHYVQLRPP-- 313
DB 278 SVNIRELKLNVVFPFRCLLVQRCGNCGCGTGNRSCTNSGKTVKYHYVQLRPPGH 337
QY 314 -KTGVKGLHSLTDVALEHEECDCVC 339
DB 338 IKRGRKTNVLDIQLDHERCDDIC 364
RESULT 3
JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N:Alternate names: Bone morphogenic protein 1
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C:Accession: JC2218
R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
A:Reference number: JC2218; MUID:94085787; PMID:8262384
A:Accession: JC2218
A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: GB:L12249; NID:9406540; PIDN:AAAL6313.1; PID:9406541
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; zinc
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: complement 1r/1s-like repeat
F:285-397/Region: complement 1r/1s-like repeat
F:285-394/Domain: C1r/C1s repeat homology <C1R1>
F:398-510/Region: complement 1r/1s-like repeat
F:398-507/Domain: C1r/C1s repeat homology <C1R2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement 1r/1s-like repeat
F:554-663/Domain: C1r/C1s repeat homology <C1R3>
F:62,105,295,326/Binding site: carbohydate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 10.3%; Score 191; DB 2; Length 707;
Best Local Similarity 45.2%; Pred. No. 6.7e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;
QY 55 NGSIIHSPKFPHTYPRNMVLVAVDENVRQLTDFERFGLDEPDDEDDICKYDFVEVEE- 113
DB 562 NGSINSPGWPKPEYPPNKNICWLVAPTQ-YRISLKFQD---FETEGNDVCKYDFVEVRSG 617
QY 114 -PSDGSVLGRWCGSGTVPKGQTSKGNHIRFVSDYFPPSEPGF 156
DB 618 LTSDSLKHGFCGS-ELPAVITSQYNNMRIFKSDNTV-SKKGF 659
RESULT 4
AS8788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N:Alternate names: bone morphogenic protein splice form BMP-1/HIS
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; AS8788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He
Science 242, 1528-1534, 1998
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, EKRALQPPRGPHQLKRVCKRNETPO' <WOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AA51833.1; PID:G179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enc
A:Reference number: AS8788; MUID:95096114; PMID:7798260
A:Accession: AS8788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:L35278; NID:G619423; PIDN:AAC41703.1; PID:G619424
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F:130-321/Domain: astacin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:738-752/Region: histidine-rich
F:91,142,332,363,599/Binding site: carbohydate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-6
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 10.3%; Score 190; DB 1; Length 823;
Best Local Similarity 36.0%; Pred. No. 9.9e-08;
Matches 54; Conservative 20; Mismatches 48; Indels 28; Gaps 7;
QY 55 NGSIIHSPKFPHTYPRNMVLVAVDENVRQLTDFERFGLDEPDDEDDICKYDFVEVEE- 113
```





Db 1089 HFTDFTLEDYFGSCQVDFVEI-RDGGYE-TSPLVG---IY--CGSVLPPTIISHGNKLWL 1141  
QY 249 -----SCTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCQVPRKVT 302  
Db 1142 KFKSDAALTAKGFS-----YWDGS--STGCGN---LTPTGVLTSFNYPM 1183  
QY 303 KKYHE---VLQRPRTYGVKGLHSITDVALEHHEC 335  
Db 1184 PYTHSSECYWRLEASHG-SPFLEFQDFLHHPSC 1218  
RESULT 11  
A5362  
procollagen I C-proteinase enhancer protein precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999  
C:Accession: A53362  
R:Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Shaw  
J. Biol. Chem. 269, 26280-26285, 1994  
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, R  
A:Reference number: A53362; MUID:95014462; PMID:7523404  
A:Accession: A53362  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-449 <TAK>  
A:Cross-references: GB:L33799; NID:g642907; PIDN:AAA61949.1; PID:g642908  
C:Genetics:  
A:Gene: GDB:PCOLCE  
A:Cross-references: GDB:305468; OMIM:600270  
A:Map position: 7q21.3-7q22  
C:Superfamily: Clr/Cls repeat homology  
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-449/Product: #status predicted <MAT>  
F:37-146/Domain: Clr/Cls repeat homology <Clr1>  
F:159-270/Domain: Clr/Cls repeat homology <Clr2>  
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:29,431/Binding site: carbonydrate (Asn) #status predicted  
Query Match 8.5%; Score 158; DB 2; Length 449;  
Best Local Similarity 34.5%; Pred. No. 2.2e-05;  
Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;  
QY 56 GSIHSPKPHPT-YPRNMLVRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEV--- 111  
Db 168 GTLTTPNPESDYPGICSMWHIAPPDQV-IATLF-EKFDLE--PDTCRYDSVSFVNG 223  
QY 112 BEPDSGLVRWCWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIM----- 164  
Db 224 AVSDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281  
QY 165 --PQVTTTSPSV-LPPSS 180  
Db 282 QGPGKRGTEPKVKLPKPS 300  
RESULT 12  
A39288  
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanoga  
C:Species: Drosophila melanogaster  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A39288  
R:Shmueli, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.  
Cell 67, 469-481, 1991  
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone  
A:Reference number: A39288; MUID:92034970; PMID:1840509  
A:Accession: A39288  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1057 <SHI>  
A:Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306  
C:Genetics:  
A:Gene: FlyBase:tlld

A:Cross-references: FlyBase:FBgn0003719  
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls rei  
C:Keywords: duplication; hydrolase; metalloproteinase; zinc  
F:136-329/Domain: astacin homology <AST>  
F:352-464/Domain: Clr/Cls repeat homology <Clr1>  
F:468-578/Domain: Clr/Cls repeat homology <Clr2>  
F:585-620/Domain: EGF homology <EG1>  
F:624-740/Domain: Clr/Cls repeat homology <Clr3>  
F:747-782/Domain: EGF homology <EG2>  
F:787-896/Domain: Clr/Cls repeat homology <Clr4>  
F:900-1013/Domain: Clr/Cls repeat homology <Clr5>  
F:221,225,231,280/Binding site: zinc (His, His, Tyr) #status predicted  
F:222/Active site: Glu #status predicted  
Query Match 8.3%; Score 153; DB 1; Length 1057;  
Best Local Similarity 33.3%; Pred. No. 0.00018;  
Matches 47; Conservative 28; Mismatches 54; Indels 12; Gaps 7;  
QY 13 LAGQRTGTRAENLSKQLQSSDKQNGVQDPRHERV----VTISNGSIHSPKPHPTYP 68  
Db 432 VSGEVITTTQTSRMLLYVNRNAAGYRGPK-ARFEVVCGLKLTQDQSIDSPNYPMDYM 490  
QY 69 RNMLVRLVAVDENVRQLTFDERFGLDEPDDICKYDFVVEE--PSDGSVLGRWCWS 126  
Db 491 PKRCVWRITAPD-NHQVALKF-QSFELE--KHDGCAIDFVEIRDGNHSDRLIGRFGD 546  
QY 127 GTVPKQTSKGNHIRIRFVSD 147  
Db 547 KLPPNIKT-RSNQWIRFVSD 566  
RESULT 13  
T30337  
polyprotein - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 03-Feb-2003  
C:Accession: T30337  
R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.  
submitted to the EMBL Data Library, March 1998  
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from  
A:Reference number: Z20829  
A:Accession: T30337  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1524 <YAN>  
A:Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1  
C:Superfamily: tryosin related polypeptide; trypsin homology  
Query Match 8.0%; Score 147.5; DB 2; Length 1524;  
Best Local Similarity 28.7%; Pred. No. 0.00082;  
Matches 54; Conservative 34; Mismatches 73; Indels 27; Gaps 10;  
QY 56 GSIHSPKPHPTYPNMLVRLVAVDENVRQLTFDERFGLDEPDDICKYDFVEV-EEP 114  
Db 439 GMIYSPNYPDPYPRKLTCSW-IIEAPENHIVKLFED-FNVEYHG--CIYDAVEYDGA 494  
QY 115 SDGSVLGRWCWCGSGTVPKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQ-----VT 168  
Db 495 BEKQLIARLCGY-TLPLPISSENPENTMLIRFKTD-MENSYPGFKVPSFVPEKQFSLPVD 552  
QY 169 ETTSPSVLPSSLSLDLNNV-VTAFSTLEELIRYLEPD-----RWQVDL-----DS 214  
Db 553 DPTTISMLHPRALDVCGMAPMTPKWMLPRIVGGEEASPNWPNQVQVIFLRTFCEGA 612  
QY 215 LVKPTWQL 222  
Db 613 IISPOWIL 620  
RESULT 14  
A59271  
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human  
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)

C:Species: Homo sapiens (man)  
 C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
 C:Accession: A59271  
 R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laursen, S.B.; Poulsen, K.  
 Nature 386, 506-510, 1997  
 A:Title: A second serine protease associated with mannan-binding lectin that activates complement factor F1-17/Domains: signal sequence #status predicted <SIG>  
 A:Reference number: A59271; MUID:97242412; PMID:9087411  
 A:Accession: A59271  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-686 <JEN>  
 A:Cross-references: GB:Y09926; NID:94007626; PIDN:CAA71059.1; PID:94007627  
 A:Experimental source: tissue liver  
 A:Note: submitted to GenBank, December 1996  
 A:Note: parts of this sequence, including the amino end of the mature protein, were determined by N-terminal sequencing  
 C:Genetics:  
 A:Gene: GDB:MASP2  
 A:Cross-references: GDB:6071500  
 A:Map position: lp36.2-1p36.3  
 C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H repeat homology; complement pathway; duplication; hydrolase; serine protease  
 C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine protease  
 F:1-15/Domains: signal sequence #status predicted <SIG>  
 F:16-444, 445-686/Product: Ra-reactive factor 2 #status predicted <MAT>  
 F:19-134/Domains: C1r/C1s repeat homology <C1R1>  
 F:142-180/Domains: EGF homology <EGF>  
 F:184-293/Domains: C1r/C1s repeat homology <C1R2>  
 F:300-361/Domains: complement factor H repeat homology <FH1>  
 F:366-430/Domains: complement factor H repeat homology <FH2>  
 F:445-679/Domains: trypsin homology <TRY>  
 F:72-90, 142-156, 152-165, 167-180, 184-211, 241-259, 300-348, 328-361, 366-412, 396-430, 434-552, 552-553, 554-555, 556-557, 558-559, 560-561, 562-563, 564-565, 566-567, 568-569, 570-571, 572-573, 574-575, 576-577, 578-579, 580-581, 582-583, 584-585, 586-587, 588-589, 590-591, 592-593, 594-595, 596-597, 598-599, 600-601, 602-603, 604-605, 606-607, 608-609, 610-611, 612-613, 614-615, 616-617, 618-619, 620-621, 622-623, 624-625, 626-627, 628-629, 630-631, 632-633, 634-635, 636-637, 638-639, 640-641, 642-643, 644-645, 646-647, 648-649, 650-651, 652-653, 654-655, 656-657, 658-659, 660-661, 662-663, 664-665, 666-667, 668-669, 670-671, 672-673, 674-675, 676-677, 678-679, 680-681, 682-683, 684-685, 686-687, 688-689, 690-691, 692-693, 694-695, 696-697, 698-699, 700-701, 702-703, 704-705, 706-707, 708-709, 710-711, 712-713, 714-715, 716-717, 718-719, 720-721, 722-723, 724-725, 726-727, 728-729, 730-731, 732-733, 734-735, 736-737, 738-739, 740-741, 742-743, 744-745, 746-747, 748-749, 750-751, 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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:48 ; Search time 8.55655 Seconds  
(without alignments)  
1896.117 Million cell updates/sec

Title: US-09-852-209A-7

Perfect score: 1848

Sequence: 1 MLLGLLLTSLALAGQRTGT.....DVALEHHECDVCVRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	10.3	707	1	BMP1_XENLA
2	183.5	9.9	928	1	NRP1_XENLA
3	181	9.8	986	1	BMP1_HUMAN
4	181	9.8	991	1	BMP1_MOUSE
5	176	9.5	923	1	NRP1_HUMAN
6	174	9.4	1022	1	TLD_BARE
7	172	9.3	922	1	NRP1_RAT
8	169	9.1	923	1	NRP1_MOUSE
9	167	9.0	914	1	NRP1_CHICK
10	163.5	8.8	616	1	SPAN_STRPU
11	158	8.5	449	1	PCO1_HUMAN
12	155.5	8.4	925	1	NRP2_RAT
13	155.5	8.4	931	1	NRP2_HUMAN
14	155.5	8.4	931	1	NRP2_MOUSE
15	153.5	8.3	326	1	VEGD_RAT
16	153	8.3	1057	1	TLD_DROME
17	147.5	8.0	704	1	CEAR_MOUSE
18	145.5	7.9	686	1	MAS2_HUMAN
19	144.5	7.8	597	1	Bp10_PARLI
20	144	7.8	699	1	CEAR_HUMAN
21	137.5	7.4	705	1	CLAR_HUMAN
22	136.5	7.4	468	1	PCO1_RAT
23	136	7.4	354	1	VEGD_HUMAN
24	135.5	7.3	358	1	VEGD_MOUSE
25	133.5	7.2	368	1	PCO1_MOUSE
26	132	7.1	415	1	VEGC_MOUSE
27	130	7.0	639	1	BMPH_STRPU
28	128	6.9	277	1	TS66_HUMAN
29	127	6.9	419	1	VEGC_HUMAN
30	125.5	6.8	245	1	PDGB_FELCA
31	123	6.7	275	1	TSG6_MOUSE
32	117.5	6.4	276	1	TSG6_RABIT
33	114.5	6.2	226	1	PDGA_XENLA

## RESULT 1

ID	BMP1_XENLA	STANDARD;	PRT;	707 AA.
AC	P98070;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OK	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=94085787; PubMed=8262384;			
RA	Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;			
RT	"Cloning and expression of cDNA encoding Xenopus laevis bone			
RT	morphogenetic protein-1 during early embryonic development."			
RL	Gene 134:257-261(1993).			
CC	-!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER			
CC	DIFFERENTIATION OF DEVELOPING ORGANS.			
CC	-!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED			
CC	TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.			
CC	-!- SIMILARITY: Contains 1 EGF-like domain.			
CC	-!- SIMILARITY: Contains 3 CUB domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
EMBL	L12249; AAA16313.1; -			
PIR	JC2218; JC2218.			
DR	HSSP; P00736; 1APO.			
DR	MEROPS; M12.005; -			
DR	InterPro; IPR001506; Astacin.			
DR	InterPro; IPR000152; Abx_hydroxyl.			
DR	InterPro; IPR000859; CUB domain.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR006209; EGF-like.			
DR	InterPro; IPR006026; Nzn_Mtpeptase.			
DR	InterPro; IPR006025; Zn_Mtpeptase.			
DR	Pfam; PF01400; Astacin; 1.			
DR	Pfam; PF00431; CUB; 3.			
DR	Pfam; PF00008; EGF; 1.			
DR	PRINTS; PR00480; ASTACIN.			
DR	SMART; SM00042; CUB; 3.			
DR	SMART; SM00179; EGF_CA; 1.			
DR	SMART; SM00235; ZnMG; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			

34	113	6.1	695	1	CASP_MESAU
35	112.5	6.1	241	1	PDGB_HUMAN
36	111.5	6.0	164	1	VEGA_CAVPO
37	111.5	6.0	226	1	TSIS_SMSAV
38	109	5.9	855	1	ST14_HUMAN
39	108.5	5.9	148	1	VEGH_ORFN7
40	105.5	5.7	207	1	VEGH_HUMAN
41	104	5.6	514	1	UVS2_XENLA
42	103.5	5.6	207	1	VEGB_BOVIN
43	103.5	5.6	225	1	PDGB_RAT
44	103.5	5.6	241	1	PDGB_SHEEP
45	103	5.6	211	1	PDGA_HUMAN

## ALIGNMENTS

P15156	mesocricetu
P01127	homo sapien
P26617	cavia porce
P01128	simian sarc
Q9756	homo sapien
P52585	orf virus (
P49765	homo sapien
P42664	xenopus lae
Q9X849	bos taurus
Q05028	rattus norv
Q95229	ovis aries
P04085	homo sapien

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DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP ? 83
FT CHAIN 84 707 POTENTIAL.
FT DOMAIN 84 284 BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 285 397 METALLOPROTEASE.
FT DOMAIN 398 509 CUB 1.
FT DOMAIN 510 551 CUB 2.
FT DOMAIN 554 666 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT METAL 176 177 CUB 3.
FT ACT SITE 177 177 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 180 180 BY SIMILARITY.
FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 146 149 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 522 525 BY SIMILARITY.
FT DISULFID 537 550 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC9B8D CRC64;

Query Match 10.3%; Score 191; DB 1; Length 707;
Best Local Similarity 45.2%; Pred. No. 6.9e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIHSKPPHTYPRNMVLVAVDENVRQLTDFDERFGLDEDDICKYDFVEVER- 113
DB 562 NGSIHSPGPKYPPNKNIGWLVAPTO-QYRSLKFDQ---PTEGNDVCKYDFVEVRSG 617
QY 114 -PSDGSVLGRWCGSGTVPGKQSKGNHIRFVSDYFPPSPG 156
DB 618 LTSDSKLHGKFGS-ELPAVITSQNNMIEFKSDNTV-SKKG 659

RESULT 2
NRPI_XENLA
ID NRPI_XENLA STANDARD; PRT; 928 AA.
AC P28824;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neupilin-1 precursor (A5 protein) (A5 antigen).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91337458; PubMed=1908252;
RA Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
RT "The A5 antigen, a candidate for the neuronal recognition molecule,
RT has homologues to complement components and coagulation factors.";
RL Neuron 7:295-307(1991).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SENAPHORINS (BY
CC SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION
CC BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER

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CC NEURONS.
CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC
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CC
CC EMBL; D10467; BAA01260.1; -.
CC HSSP; P12259; 1CZT
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR000421; FAS8_C.
CC InterPro; IPR000998; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FAS8C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FAS8C_1; 2.
CC PROSITE; PS01286; FAS8C_2; 2.
CC PROSITE; PS00022; FAS8C_3; 2.
CC PROSITE; PS00740; MAM 1; 1.
CC PROSITE; PS00060; MAM 2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Antigen.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 928 NEUROFILIN-1.
FT DOMAIN 22 860 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 861 883 POTENTIAL.
FT DOMAIN 884 928 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 584 F5/8 TYPE C 2.
FT DOMAIN 646 812 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 584 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 928 AA; 103416 MW; AF6B323B0A4C789D CRC64;

Query Match 9.9%; Score 183.5; DB 1; Length 928;
Best Local Similarity 30.7%; Pred. No. 4e-07;
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;

QY 50 VTISNGSIHSPKPPHTYPRNMVLVAVDENVRQLTDFDERFGLDEDDICKYDFV 109
DB 31 IKITSPLTSAGYPSHPSPPSCQCEWLQAPHYQRIIMFNPHFDLEDR---CKYDV 87
QY 110 EV--EPPDGSVLGRWCGSGTVPGKQSKGNHIRFVSDYFPPSPGCIHYSIM--P 165
DB 88 EVIDGDNAGNQLLGKYGK-IAPSPLVSTGSPSIFIRFVSDYETPG-AGFSIRYEVFKTP 145
QY 166 QYTE--TTSPLP-----PSSLSLDLNNVATATSTLEELIRYLEPDRQVLDLS 214
DB 146 ECSRNFNTSSNGVIGPKYKPKYNALECTYIFA----PKMQEIV--LEFSEFELEADS 198

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RESULT 3
ID -BMP1_HUMAN STANDARD; PRT; 986 AA.
AC P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q99438;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
GN BMP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).
RC TISSUE=Skin;
RA MEDLINE=96209868; PubMed=8643539;
RA Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V.,
RA Prockop D.J.;
RA "The C-proteinase that processes procollagens to fibrillar collagens
RT is identical to the protein previously identified as bone morphogenic
RT protein-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).
RX MEDLINE=89072730; PubMed=3201241;
RX Wozney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,
RA Kriz R.W., Hewick R.M., Wang E.A.;
RA "Novel regulators of bone formation: molecular clones and
RT activities.";
RL Science 242:1528-1534(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
RC TISSUE=Placenta;
RX MEDLINE=96160316; PubMed=9500680;
RX Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
RA "Three alternatively spliced variants of the gene coding for the human
RT bone morphogenetic protein-1.";
RL J. Mol. Med. 76:141-146(1998).
RN [4]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).
RC TISSUE=Placenta;
RX MEDLINE=95096114; PubMed=7798260;
RX Takahara K., Lyons G.E., Greenspan D.S.;
RA "Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
RT are encoded by alternatively spliced transcripts which are
RT differentially expressed in some tissues.";
RL J. Biol. Chem. 269:32572-32578(1994).
RN [5]
RP DISULFIDE BOND IN METALLOPROTEASE DOMAIN.
RX MEDLINE=21336528; PubMed=11283002;
RX Garrigue-Antar L., Barker C., Kadler K.E.;
RA "Identification of amino acid residues in bone morphogenetic
RT protein-1 important for procollagen C-proteinase activity.";
RL J. Biol. Chem. 276:26237-26242(2001).
CC -!- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
CC AND II. INDUCES CARTILAGE AND BONE FORMATION.
CC -!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala--Asp in type I and II procollagens and at Arg--Asp in type
CC III.
CC COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
CC ENDOPEPTIDASE ENHANCER PROTEIN.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Name=BMP1-3;
CC IsoId=P13497-1; Sequence=Displayed;
CC Name=BMP1-1;
CC IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
CC Name=BMP1-2;
CC IsoId=P13497-7; Sequence=Not described;
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FT PROPEP      26      125      POTENTIAL.
FT CHAIN       126      991      BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN      126      326      METALLOPROTEASE.
FT DOMAIN      327      439      CUB 1.
FT DOMAIN      440      551      CUB 2.
FT DOMAIN      552      593      EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN      596      707      CUB 3.
FT DOMAIN      708      748      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN      752      864      CUB 4.
FT DOMAIN      865      981      CUB 5.
FT METAL       218      218      ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE    219      219      BY SIMILARITY.
FT METAL       222      222      ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL       228      228      ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID    188      191      BY SIMILARITY.
FT DISULFID    327      353      BY SIMILARITY.
FT DISULFID    380      402      BY SIMILARITY.
FT DISULFID    440      466      BY SIMILARITY.
FT DISULFID    493      515      BY SIMILARITY.
FT DISULFID    556      568      BY SIMILARITY.
FT DISULFID    564      577      BY SIMILARITY.
FT DISULFID    579      592      BY SIMILARITY.
FT DISULFID    596      622      BY SIMILARITY.
FT DISULFID    649      671      BY SIMILARITY.
FT DISULFID    712      723      BY SIMILARITY.
FT DISULFID    719      732      BY SIMILARITY.
FT DISULFID    734      747      BY SIMILARITY.
FT CARBOHYD    96      96      N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD    147      147      N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD    337      337      N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD    368      368      N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD    604      604      N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE    991 AA; 111607 MW; 68A1847783A0BB9E CRC64;

Query Match      9.8%; Score 181; DB 1; Length 991;
Best Local Similarity 42.6%; Pred. No. 6.9e-07;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

QY 55 NGSIHSPKPHPTYPYPRNMLVWLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVER- 113
Db 604 NGSIHSPGWKPEYPPNKNCKIWLVAPTQ-YRISLQFD--PFETEGNDVCKYDFVEVRSG 659

QY 114 -PSDSVLGRWCGSTVPGKQTSKGNHRIHFVSDYFSPSGFCIHY 160
Db 660 LTADSKLHGKFCGS-EKPEVITSYNNMRVPEKSDNTV-SKKGFKAHF 705

RESULT 5
NRPI_HUMAN
AC 014786; O60461; STANDARD; PRT; 923 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurophilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
GN NRPI OR NRP OR VEGF165R.
OS Homo sapiens (HUMAN).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=97433084; PubMed=9288753;
RA He Z., Tessier-Lavigne M.;
RT "Neurophilin is a receptor for the axonal chemorepellent semaphorin III."
RL Cell 90:739-751(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.
RX TISSUE=Brain;
RX MEDLINE=98188099; PubMed=9529250;
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;

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RT "Neurophilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.
RX TISSUE=Prostatic adenocarcinoma;
RX MEDLINE=20183929; PubMed=1068880;
RA Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.;
RT "Identification of a natural soluble neurophilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity."; Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20309748; PubMed=10748121;
RX Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neurophilin-2 and neurophilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neurophilin-2 functions as a receptor for the 145-amino acid form of VEGF."; J. Biol. Chem. 275:18040-18045(2000).
CC -!- FUNCTION: The membrane-bound isoform 1 is a receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsant activity of semaphorins. It binds to semaphorin 3A, The PLGF-2 isoform of PGF. The VEGF-165 isoform of VEGF and VEGF-B. Coexpression with KDR results in increased VEGF-165 binding to KDR as well as increased chemotaxis. It may regulate VEGF-induced angiogenesis.
CC -!- FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to inhibit its binding to cells. It may also induce apoptosis by sequestering VEGF-165. May bind as well various members of the semaphorin family. Its expression has an adverse effect on blood vessel number and integrity.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Membrane-bound;
CC IsoId=O14786-1; Sequence=Displayed;
CC Name=2; Synonyms=Soluble, SNRP1;
CC IsoId=O14786-2; Sequence=VSP_004339, VSP_004340;
CC -!- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not seem to overlap. Isoform 1 is expressed by the blood vessels of different tissues. In the developing embryo it is found predominantly in the nervous system. In adult tissues, it is highly expressed in heart and placenta; moderately in lung, liver, skeletal muscle, kidney and pancreas; and low in adult brain. Isoform 2 is found in liver hepatocytes, kidney distal and proximal tubules.
CC -!- SIMILARITY: BELONGS TO THE NEUROPHILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -----
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CC -----
DR EMBL; AF018956; AAC51759.1; -
DR EMBL; AF016050; AAC12921.1; -
DR EMBL; AF145712; AAF44344.1; -
DR PDB; 1KEX; 28-JAN-03.
DR GenSeq; HGNC:8004; NRPI.
DR MIM; 602059; -
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. .; TAS.
DR GO; GO:0007411; P:axon guidance; TAS.

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Qy 2 LLLGLLLTSLAGORTCTRAESNLSKQLQLSSDKQNGVQDPRHVRVVTISGNGSIHSP 61
Db 7 LCATLALALALAG-----AFRSKCGG-----TIKINPGYLTSP 42
Qy 62 KFPHTYPRNMVLRVAVDENVRITQTFDFRFGLEDPEDDICKYDFVEV--EBPSDGSV 119
Db 43 GYPHSYHSEKCEWLIQAEPYQRIINFNPHFDLEDRLD---CKDYVEVIDGENEGGRL 99
Qy 120 LGRWCGSTVGKQTSKGNHRIKRVSDYEPSPGFCIHYSIIM--PQVET-TSPS 174
Db 100 WKGFCGK-IAPSPVSSGPFLLIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155

RESULT 8
NRPI_MOUSE
ID NRPI_MOUSE STANDARD; PRT; 923 AA.
AC P97333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (A5 protein).
GN NRPI OR NRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BAUB/C; TISSUE=Embryonic brain;
RX MEDLINE=96353149; PubMed=8748368;
RA Kawakami A., Kitukawa T., Takagi S., Fujisawa H.;
RT "Developmentally regulated expression of a cell surface protein,
RT neuropilin, in the mouse nervous system.";
RL J. Neurobiol. 29:1-17(1996).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF EGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50086; BAA08789.1; -.
DR HSSP; P12259; 1CZT.
DR MGD; MGI:106206; Nrp.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 2.

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DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00222; FA58C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00600; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 923 NEUROPILIN-1.
FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 857 879 POTENTIAL.
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 147 265 CUB 1.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 923 AA; 103020 MW; 0644B8A170796808 CRC64;

Query Match 9.1%; Score 169; DB 1; Length 923;
Best Local Similarity 31.5%; Pred. No. 6e-06;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;

Qy 2 LLLGLLLTSLAGORTCTRAESNLSKQLQLSSDKQNGVQDPRHVRVVTISGNGSIHSP 61
Db 7 LCATLALALALAG-----AFRSKCGG-----TIKINPGYLTSP 42
Qy 62 KFPHTYPRNMVLRVAVDENVRITQTFDFRFGLEDPEDDICKYDFVEV--EBPSDGSV 119
Db 43 GYPHSYHSEKCEWLIQAEPYQRIINFNPHFDLEDRLD---CKDYVEVIDGENEGGRL 99
Qy 120 LGRWCGSTVGKQTSKGNHRIKRVSDYEPSPGFCIHYSIIM--PQVET-TSPS 174
Db 100 WKGFCGK-IAPSPVSSGPFLLIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155

RESULT 9
NRPI_CHICK
ID NRPI_CHICK STANDARD; PRT; 914 AA.
AC P97795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (A5 protein).
GN NRPI OR NRP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=White leghorn; TISSUE=Embryonic brain;
RX MEDLINE=95324761; PubMed=7601310;
RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,
RA Fujisawa H.;
RT "Expression of a cell adhesion molecule, neuropilin, in the
RT developing chick nervous system.";
RL Dev. Biol. 170:207-222(1995).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY

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FT METAL          200      ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID       299      BY SIMILARITY.
FT DISULFID       305      BY SIMILARITY.
FT DISULFID       319      BY SIMILARITY.
SQ SEQUENCE       616 AA; 67902 MW; 397CD923FFB9B98 CRC64;
Query Match      8.8%; Score 163.5; DB 1; Length 616;
Best Local Similarity 28.0%; Pred. No. 1e-05;
Matches 63; Conservative 30; Mismatches 85; Indels 47; Gaps 11;

QY 9 LTSALAGQRTG-TRAESNLSSKLQSSDKE-----QNGVQDPRHRRVV--TISGN- 55
Db 269 LNSRL-GORTLSAADIELANRIYECDDVEDCSNDECLNGYHDADCDVCPSSVSGDL 327
QY 56 -----GSIHSKPPHYPRNVLVRLVAVDENVRIQLTFDERF 94
Db 328 QDGGPTVRPDCSRFTMTGRTISPNPSYDNTACVIEG-PYGSTIELTF---L 383
QY 95 GLEDPEDDICKYDFVEEPPSPGVLGRWCGSTVGKQTSKGNHIRIFVSDYFPPS-- 152
Db 384 DMEIETETLCRYDAVEVRKDDINSIGKPCGN-TLPPVQISSNQMVSTSD---PSIT 439
QY 133 EPGFCIHVSIIMPQVT--ETTSFVLPSSLSLDLNNAVTAFST 195
Db 440 RRGFKATYVILIIQTTFVSTTTLQTPPTTTLQTNPNSTTLQT 484

RESULT 11
PCOI_HUMAN
ID PCOI_HUMAN STANDARD; PRT; 449 AA.
AC Q15113; O14550;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (type 1 procollagen C-
DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler E., Binianinov L., Brusel M., Eddy R.L.,
RA Jani-Sait S., Shows T.B., Greenspan D.S.;
RT "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RL J. Biol. Chem. 269:26280-26285(1994).
RN [2]
RP REVISIONS TO 56; 154 AND 373.
RA Kessler E.;
RL Unpublished observations (FEB-2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.;
RT "Smooth muscle cell derived procollagen C-protease enhancer protein.";
RL Cell Struct. Funct. 21:662-662(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Glockner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.;
RT "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
RT reveals 17 genes.";
RL Genome Res. 8:1060-1073(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99134301; PubMed=9933570;
RA Scott L.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
RT "Structural organization and expression patterns of the human and
RT mouse genes for the type I procollagen COOH-terminal proteinase
RT enhancer protein.";
RL Genomics 55:229-234(1999).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altshuler R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klatchuk S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
RX MEDLINE=20092317; PubMed=10625689;
RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
RA Banda M.J.;
RT "Post-translational proteolytic processing of procollagen C-terminal
RT proteinase enhancer releases a metalloproteinase inhibitor.";
RL J. Biol. Chem. 275:1384-1390(2000).
CC -!- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE I
CC PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
CC -!- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN
CC METALLOPROTEINASE INHIBITORY ACTIVITY.
CC -!- SUBCELLULAR LOCATION. Secreted.
CC -!- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 1 NTR domain.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; L33799; AAA61949.1; ALT_SEQ.
CC EMBL; AB008549; BAA32281.1; -
CC EMBL; AF033356; AAC78800.1; -
CC EMBL; AF083655; AAC16041.1; -
CC EMBL; BC000574; AAH00574.1; -
CC EMBL; BC033205; AAH33205.1; -
CC EMBL; HGNC:8738; PCOLCE.
CC MIM; 600270; -
CC GO; GO:0008151; P:cell growth and/or maintenance; TAS.
CC GO; GO:0007275; P:development; TAS.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR001134; Netrin_C.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF01759; NTR; 1.
CC SMART; SM00643; C345C; 1.
CC SMART; SM00042; CUB; 2.

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DR PROSITE; PS01180; CUB; 2.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 449 PROCOLLAGEN C-PROTEINASE ENHANCER
FT CHAIN 26 449 PROTEIN.
FT DOMAIN 37 149 CUB 1.
FT DOMAIN 159 273 CUB 2.
FT DOMAIN 329 438 NTR.
FT SITE 287 288 CLEAVAGE.
FT SITE 288 289 CLEAVAGE.
FT SITE 289 289 CLEAVAGE.
FT SITE 293 294 CLEAVAGE.
FT SITE 299 300 CLEAVAGE.
FT SITE 303 304 CLEAVAGE.
FT SITE 303 304 CLEAVAGE.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 449 AA; 47972 MW; 3D88430158648796 CRC64;

Query Match 8.5%; Score 158; DB 1; Length 449;
Best Local Similarity 34.5%; Pred. No. 1.9e-05;
Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;

QY 56 GSIHSPKFPHT-YPRNMLVWRLVAVDENVRIQLTFDERFGLDEDDICKYDFVEV--- 111
Db 168 GTLTTPNPFESDYPPGISCWHIAPPQV-IALTF-EKPLE--PDYCYRDSVSFVNG 223
QY 112 BEPSDGSVLGRCGSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIM----- 164
Db 224 AVSDSRRLGRKFCGD-AVPGSISSEGNELLQVFSVDSLVTAD-GFSASYKTLPRGTAKEG 281
QY 165 --PQWETTSFV-LPPSS 180
Db 282 QGPGKRGTEPKVKLPPKS 300

RESULT 12
NRP2_RAT STANDARD; PRT; 925 AA.
AC O35276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neupilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
FA Ginty D.D.;
RT "Neupilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE
CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
CC LINING IN THE RIBS.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
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CC EMBL; AF016297; AAC53338.1; -.
DR HSSP; P12259; 1CZT.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FAS5 C.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS5C; 2.
DR SMART; SM01137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS5C_1; 2.
DR PROSITE; PS01286; FAS5C_2; 2.
DR PROSITE; PS00222; FAS5C_3; 2.
DR PROSITE; PS00060; MAM_2; 1.
DR Transmembrane; Glycoprotein; Neutrone; Signal; Repeat; Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 925 NEUROPILIN-2.
FT DOMAIN 23 858 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 859 883 POTENTIAL.
FT DOMAIN 884 925 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DISULFID 88 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CRC64;

Query Match 8.4%; Score 155.5; DB 1; Length 925;
Best Local Similarity 33.3%; Pred. No. 7.5e-05;
Matches 41; Conservative 19; Mismatches 56; Indels 7; Gaps 4;

QY 42 QDPRHERVVTISNGSIHSPKFPHTYPRNMLVWRLVAVDENVRIQLTFDERFGLDEPDED 101
Db 24 QDPPCGRLNSKDAGYITSPGYPDYPSHQNCWVYVAPENPQKIVLNFNPFIEKHDD- 82
QY 102 DICKYDFVEEPEPSDGS--VLGRWCGSGTVPCKQTSKGNHIRFVSDYFPPSEPGFCIH 159
Db 83 --CKYDFEIRDDGDSADLLQKHCN-IAPTTIISGSLVLYIKTSD-YARQAGFSLR 138
QY 160 YSI 162
Db 139 YEI 141

RESULT 13
NRP2_HUMAN STANDARD; PRT; 931 AA.
AC O60462; O14820; O14821;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neupilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRP2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CC NCBI\_TaxID=9606;  
RN [1] SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).  
RX MEDLINE=97470888; PubMed=9331348;  
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema  
RT III.";  
RL Neuron 19:547-559(1997).  
RN [2] SEQUENCE FROM N.A. (ISOFORM A22).  
RP TISSUE=Brain;  
RX MEDLINE=98180099; PubMed=9529250;  
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;  
RT "Neuropilin-1 is expressed by endothelial and tumor cells as an  
RT isoform-specific receptor for vascular endothelial growth factor.";  
RL Cell 92:735-745(1998).  
RN [3] CHARACTERIZATION.  
RX MEDLINE=20309748; PubMed=10748121;  
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;  
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid  
RT form of vascular endothelial growth factor (VEGF) and of placenta  
RT growth factor-2, but only neuropilin-2 functions as a receptor for  
RT the 145-amino acid form of VEGF.";  
RL J. Biol. Chem. 275:18040-18045(2000).  
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165  
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.  
CC -!- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH  
CC NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=A22;  
CC IsoId=060462-1; Sequence=Displayed;  
CC Name=A0; Sequence=VSP\_004342;  
CC IsoId=060462-2; Sequence=VSP\_004342;  
CC Name=A17;  
CC IsoId=060462-3; Sequence=VSP\_004341;  
CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.  
CC -!- SIMILARITY: Contains 2 CUB domains.  
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.  
CC -!- SIMILARITY: Contains 1 MAM domain.  
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CC -----  
DR EMBL; AF022859; AAC51788.1; -;  
DR EMBL; AF022860; AAC51789.1; -;  
DR EMBL; AF016098; AAC12922.1; -;  
DR HSRF; F12259; 1CZT.  
DR Genew; HGNC:8005; NRP2.  
DR MIM; 602070; -;  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR GO; GO:0005021; F:vascular endothelial growth factor receptor; TAS.  
DR GO; GO:0007411; F:axon guidance; TAS.  
DR InterPro; IPR000859; CUB\_domain.  
DR InterPro; IPR000421; FA58\_C.  
DR InterPro; IPR000998; MAM\_domain.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00754; F5 F8 type\_C; 2.  
DR Pfam; PF00629; MAM; 1.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00231; FA58C; 2.  
DR SMART; SM00137; MAM; 1.  
DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; FA58C\_1; 2.  
DR PROSITE; PS01286; FA58C\_2; 2.  
DR PROSITE; PS00222; FA58C\_3; 2.  
DR PROSITE; PS00060; MAM\_2; 1.  
KW Transmembrane; Glycoprotein; Neuropeptide; Signal; Repeat; Receptor;  
FT SIGNAL 1 20 OR 22 (POTENTIAL).  
FT CHAIN 21 931 NEUROFILIN-2.  
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 865 889 POTENTIAL.  
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 28 142 CUB 1.  
FT DOMAIN 149 267 CUB 2.  
FT DOMAIN 277 427 F5/8 TYPE C 1.  
FT DOMAIN 334 592 F5/8 TYPE C 2.  
FT DOMAIN 434 592 MAM.  
FT DOMAIN 642 802 POLY-SER.  
FT DOMAIN 671 674 BY SIMILARITY.  
FT DISULFID 28 55 BY SIMILARITY.  
FT DISULFID 83 105 BY SIMILARITY.  
FT DISULFID 149 175 BY SIMILARITY.  
FT DISULFID 208 230 BY SIMILARITY.  
FT DISULFID 277 427 BY SIMILARITY.  
FT DISULFID 434 592 BY SIMILARITY.  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 629 629 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 839 839 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 809 813 Missing (in isoform A17).  
FT VARSPLIC 809 830 Missing (in isoform A0).  
FT CONFLICT 602 602 /FTID=VSP\_004342.  
FT SEQUENCE 931 AA; 104830 MW; 270CBAB69A0A797C CRC64;  
Query Match 8.4%; Score 155.5; DB 1; Length 931;  
Best Local Similarity 32.1%; Pred. No. 7.6e-05;  
Matches 42; Conservative 20; Mismatches 62; Indels 7; Gaps 4;  
QY 34 SDKQNGVQDPRHVRVTTISNGSIHSPKFTHTYPRNVLVAVDENVRILQTFEDER 93  
DB 16 SRHQVQGPDPCCGRILNSKDAGYITSGYQDYPHONCEWIVYAPENQKIVLNFPH 75  
QY 94 FGLEDPEDDICKYDFVEVEPEFSDGS--VLGRWCGSGTVPGRQTSKGNHIRFVSDYFP 151  
DB 76 FEIEKHD--CKYDFIEIRDGSEADLGRKCGN-IAPPTIISGSMYIKFTSD-YAR 130  
QY 152 SEPGFCHYSI 162  
DB 131 QGAGFSURYEI 141  
RESULT 14  
NRP2\_MOUSE  
ID NRP2\_MOUSE STANDARD; PRT; 931 AA.  
AC 035375; 035373; 035374; 035376; 035377; 035378;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165  
DE receptor 2).  
GN NRP2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1] SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).  
RP STRAIN=BA1B/C;  
RX MEDLINE=97470888; PubMed=9331348;  
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema  
RT III.";

Neuron 19:547-559(1997).

CC -|- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165  
 CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.

CC -|- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH  
 CC NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.

CC -|- SUBCELLULAR LOCATION: Type 1 membrane protein.

CC -|- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=6;

CC Name=A22;

CC IsoId=035375-1; Sequence=Displayed;

CC Name=A0;

CC IsoId=035375-2; Sequence=VSP\_004344;

CC Name=A5;

CC IsoId=035375-3; Sequence=VSP\_004345;

CC Name=A17;

CC IsoId=035375-4; Sequence=VSP\_004343;

CC Name=B0;

CC IsoId=035375-5; Sequence=VSP\_004346;

CC Name=B5;

CC IsoId=035375-6; Sequence=VSP\_004347;

CC -|- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME  
 CC NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,  
 CC INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.

CC -|- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS  
 CC DEVELOPMENTALLY REGULATED.

CC -|- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -|- SIMILARITY: Contains 2 CUB domains.

CC -|- SIMILARITY: Contains 2 F5/8 type C domains.

CC -|- SIMILARITY: Contains 1 MAM domain.

CC -----

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CC -----

DR EMBL; AF022856; AAC53379.1; -  
 DR EMBL; AF022854; AAC53377.1; -  
 DR EMBL; AF022855; AAC53378.1; -  
 DR EMBL; AF022857; AAC53380.1; -  
 DR EMBL; AF022858; AAC53381.1; -  
 DR EMBL; AF022861; AAC53382.1; -  
 DR HSSP; P12259; LCZT.  
 DR MGD; MGI:1100492; Nrp2.  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000421; FA58 C.  
 DR InterPro; IPR000998; MAM domain.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam; PF00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FA58C; 2.  
 DR SMART; SM0137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FA58C 1; 2.  
 DR PROSITE; PS01286; FA58C 2; 2.  
 DR PROSITE; PS50022; FA58C 3; 2.  
 DR PROSITE; PS50060; MAM 2; 1.  
 DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;  
 KW Alternative splicing.

FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 931 NEUROFILIN-2.  
 FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 865 889 POTENTIAL.  
 FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 149 267 CUB 1.  
 FT DOMAIN 277 427 CUB 2.  
 FT DOMAIN 434 592 F5/8 TYPE C 1.  
 FT DOMAIN 434 592 F5/8 TYPE C 2.  
 FT DOMAIN 642 802 MAM.

FT DOMAIN 838 845 POLY-SER.  
 FT DISULFID 28 55 BY SIMILARITY.  
 FT DISULFID 83 105 BY SIMILARITY.  
 FT DISULFID 149 175 BY SIMILARITY.  
 FT DISULFID 208 230 BY SIMILARITY.  
 FT DISULFID 277 427 BY SIMILARITY.  
 FT DISULFID 434 592 BY SIMILARITY.  
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 839 839 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 809 813 Missing (in isoform A17).  
 FT VARSPLIC 809 830 Missing (in isoform A0).  
 FT VARSPLIC 814 830 Missing (in isoform A5).  
 FT VARSPLIC 810 931 Missing (in isoform B0).  
 FT VARSPLIC 814 931 Missing (in isoform B5).  
 FT CONFLICT 786 786 G -> I (IN REF. 1; AAC53380/AAC53381).  
 FT SEQUENCE 931 AA; 104558 MW; 76F2443F411D2F63 CRC64;  
 SQ  
 Query Match 8.4%; Score 155.5; DB 1; Length 931;  
 Best Local Similarity 32.8%; Pred. No. 7.6e-05;  
 Matches 43; Conservative 18; Mismatches 63; Indels 7; Gaps 4;

QY 34 SDKEQGVQDPRHERVVTISGNSTHSPKFFPHYTPRNMLVWRLVAVDENVRIQLTFDER 93  
 DB 16 SGHEVRSQDPPCGGRPNKDAGYITSPGYQDYFQHCNCEWIVYAPENQKIVLNFPH 75  
 QY 94 FGLEDPEDDICKYDFVVEBPDSGS--VLGRWCGSGTVPKQTSKGNHIRIFVSPDEPP 151  
 DB 76 FEIEKHD--CKYDFEIRDGDSADLLGKCGN-IAPPTISSGSVLYIKFTSD-YAR 130  
 QY 152 SEPGFCIHYSI 162  
 DB 131 QGAGFSLRYEI 141

RESULT 15  
 VEGD RAT  
 ID\_VEGD RAT STANDARD; PRT; 326 AA.  
 AC O35251;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced  
 DE growth factor) (FIGF).  
 GN FIGF OR VEGFD.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Yamada Y., Hirata Y., Nezu J., Shimane M.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC -|- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis  
 CC and endothelial cell growth, stimulating their proliferation and  
 CC migration and also has effects on the permeability of blood

Search completed: November 25, 2003, 21:02:52  
Job time : 9.55655 secs

	Query Match	8.3%; Score 153.5; DB 1; Length 326;
	Best Local Similarity	27.7%; Pred. No. 3e-05;
	Matches	56; Conservative
		28; Mismatches 81; Indels 37; Gaps 9;
Qy	155	GFCIHYSIIIMPOVETTSPSVLPSSLSLDLNNAVTAFSTLELIHYLEPDRMQV--- 210
Dd	21	GFSTEHRVKDVSLERSRSRVLERS-----EQIRAAATLELLQVAHSEDKMLWRCR 73
Qy	211	-----DLDSLYKPTWOLLGKAFLYGHKKSKVMNLILKEEVKYIYSTPRNFVSIREEL 263
Dd	74	LKLKSLANVDTSRSTRSREPAATFYDTET----LKVIDEEMORTQCSPRETCVEVASSEL 129
Qy	264	-KRDTDTTFWPCLLVKRCGGNCACCLHNCEQCVPRK--VTKKYHEVLQRPKTKGVKG 319
Dd	130	GKTINTFTFKPCVVNVFRCGG---CC-NEEESVMCMNTSTSISKQLFEISV-PLTSV-- 180
Qy	320	LHKSLTDVALEHHBEEDCVCKRG 341
Dd	181	--PELVPPVKIANHTGCCKLPTG 200



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:58:59 ; Search time 30.4613 Seconds  
(without alignments)  
2922.663 Million cell updates/sec

Title: US-09-852-209a-7

Perfect score: 1848

Sequence: 1 MLLGLLLTALAGQRTGT.....DVALEHHBECVCVCKGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues 830525

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL 23.\*
- 2: sp\_archaea.\*
- 3: sp\_bacteria.\*
- 4: sp\_fungi.\*
- 5: sp\_human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mammal.\*
- 8: sp\_mhc.\*
- 9: sp\_organelle.\*
- 10: sp\_phage.\*
- 11: sp\_plant.\*
- 12: sp\_rodent.\*
- 13: sp\_virus.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	11 Q9QY71	Q9QY71 mus musculus
2	1846	99.9	345	11 Q8C119	Q8C119 mus musculus
3	1819	98.4	345	11 Q9JH8	Q9JH8 mus musculus
4	1801	97.5	345	11 Q9EQX6	Q9EQX6 rattus norv
5	1867	90.2	345	4 Q9UL22	Q9UL22 homo sapien
6	1864	90.0	345	4 Q9NRA1	Q9NRA1 homo sapien
7	1552	84.0	345	13 Q9I946	Q9I946 gallus gall
8	1375	74.4	258	11 Q8K429	Q8K429 rattus norv
9	754	40.8	370	11 Q9EQT1	Q9EQT1 rattus norv
10	752	40.7	370	4 Q9CZP0	Q9CZP0 homo sapien
11	750.5	40.6	364	4 Q9BWV5	Q9BWV5 homo sapien
12	746.5	40.4	370	11 Q92517	Q92517 mus musculus
13	440.5	23.8	261	11 Q8K213	Q8K213 mus musculus
14	201	10.9	923	13 Q9QFX6	Q9QFX6 brachydanio
15	201	10.9	923	13 Q8AXP1	Q8AXP1 brachydanio
16	192.5	10.4	691	13 O57658	O57658 gallus gall

#### ALIGNMENTS

##### RESULT 1

Q9QY71 PRELIMINARY; PRT; 345 AA.

AC Q9QY71; (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)

DE Fallotain (Platelet-derived growth factor C).

GN PDGFC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

RT "cDNA cloning of fallotain from mouse ovary.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;

RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cecum, Cerebellum, and Head;

RX MEDLINE=23154683; PubMed=12466851;

RA The FANTOM Consortium,

RT The RIKEN Genome Exploration Research Group Phase I & II Team;

RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL; AF117608; AAF22516.1; -.

DR EMBL; AF266467; AAK58566.1; -.

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DR EMBL; AK033734; BAC28455.1; --
DR EMBL; AK042767; BAC31358.1; --
DR EMBL; AK052947; BAC32516.1; --
DR MGD; MGI:1859631; Pdgfc.
DR InterPro; IPR000859; CUB_domain.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTGTGTRAESNLSSKQLSSDKEQNGVQDPHREVVTTISGNGSIHS 60
DB 1 MLLGLLLTSLALAGTGTGTRAESNLSSKQLSSDKEQNGVQDPHREVVTTISGNGSIHS 60
QY 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
QY 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
QY 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
QY 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
QY 181 LSLLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
DB 181 LSLLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
QY 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQLRPKTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345

RESULT 3
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
organogenesis.";
RL Mech. Dev. 96:209-213(2000).
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MGI:1859631; Pdgfc.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 98.4%; Score 1819; DB 11; Length 345;
Best Local Similarity 98.8%; Pred. No. 1.2e-163;
Matches 341; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTGTGTRAESNLSSKQLSSDKEQNGVQDPHREVVTTISGNGSIHS 60
DB 1 MLLGLLLTSLALAGTGTGTRAESNLSSKQLSSDKEQNGVQDPHREVVTTISGNGSIHS 60
QY 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKGKTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPVTTTSPSVLPSS 180
QY 181 LSLLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
DB 181 LSLLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300

Query Match 99.9%; Score 1846; DB 11; Length 345;
Best Local Similarity 99.7%; Pred. No. 3.4e-166;
Matches 344; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTGTGTRAESNLSSKQLSSDKEQNGVQDPHREVVTTISGNGSIHS 60
DB 1 MLLGLLLTSLALAGTGTGTRAESNLSSKQLSSDKEQNGVQDPHREVVTTISGNGSIHS 60
QY 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120

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Db 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEEDCVCGRNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEEDCVCGRNAGG 345

RESULT 4
Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE Spinal cord-derived growth factor.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=1162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033830; BAB19969.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM0042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 11; Length 345;
Best Local Similarity 96.8%; Pred. No. 6.1e-162;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMVLVRLVAVDENVRIQLTFDERRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNTVLVRLVAVDENVRIQLTFDERRFGLDEPDDICKYDFVEVEEPSDGSVL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPEPGFCIHYSIMPVQTTTSPSVLPSS 180
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPEPGFCIHYSIMPVQTTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFYKKSQVNLNL 240
Db 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFYKKSQVNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300

RESULT 5
Q9UL22 PRELIMINARY; PRT; 345 AA.
ID Q9UL22
```

```
AC Q9UL22;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived
DE growth factor) (Platelet-derived growth factor C).
GN HSCDGF OR PDGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Tsai Y.J., Lee R.K.K., Lin S.P.;
RT "Fallotein, a novel growth factor like gene identified in human
RT uterus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
RN [3]
RC SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR EMBL; AF260738; AAK51637.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;
```

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.9e-149;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHERVVTISGNGSIHS 60
Db 1 MSLFGLLLLTALAGQRTGTRAESNLSSKQFSSNKQNGVQDPOHERITVTSTNGSIHS 60
QY 61 PKFPHYPRNMVLVRLVAVDENVRIQLTFDERRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PRFPHYPRNTVLVRLVAVDENVRIQLTFDERRFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEYFPEPGFCIHYSIMPVQTTTSPSVLPSS 180
Db 121 GRWCSGTVPGKQISKGNQIRIRFVSDEVFPPEPGFCIHYNIVMQFTEAVSPSVLPSS 180
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFYKKSQVNLNL 240
Db 181 LFLDLNNAITAFSTLEELIRYLEPERWQLEDLYRPTWQLLGKAFVGRKSRVVDNL 240
QY 241 LKEEVKLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300
Db 241 LTEEVRLYSCTPRNFSVSIRESLKRDTDFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300
```

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
ID Q9NRA1 PRELIMINARY; PRT; 345 AA.  
DB 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGSGTG 345

## RESULT 6

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
ID Q9NRA1 PRELIMINARY; PRT; 345 AA.  
DB 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGSGTG 345

OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA MEDLINE=20268201; PubMed=10806482;  
RX Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,  
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,  
RA Bethsholtz C., Heidin C.-H., Alitalo K., Oetman A., Eriksson U.,  
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-  
receptor.";  
RL Nat. Cell Biol. 2:302-309 (2000).  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF244813; AAF80597.1; --  
DR Genew; HGNC:8801; PDGFC.  
DR InterPro; IPR000859; CUB\_domain.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS0278; PDGF 2; 1.  
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 90.0%; Score 1664; DB 4; Length 345;  
Best Local Similarity 86.7%; Pred. No. 5.7e-149;  
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAEISLSSKQLSSDKQNGVDPHRRVVTISGNGSIHS 60  
DB 1 MSLFGLLLVTSALAGORRTQAEISLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
QY 61 PKFPHYPRNMYLVWRLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEPSPGSLV 120  
DB 61 PKFPHYPRNTVLWRLVAVDENVWQLTFDERFGLDEDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIMPOVTTTSPSVLPSS 180  
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIMVQFTTAVSPSVLPSS 180  
QY 181 LSLLDNLNNAVTAFTLEELIRYLEPDRWQVLDLSYKPTWQLLGKAFYLGKSKVYNLNL 240  
DB 181 LPLDLNNAITAFSTLEELIRYLEPDRWQVLDLSYKPTWQLLGKAFYLGKSKRVVDNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
DB 241 LTEEVRVLSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300  
QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGSGTG 345

## RESULT 7

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
ID Q91946 PRELIMINARY; PRT; 345 AA.  
AC Q91946

DT 01-OCT-2000 (TREMELrel. 15, Created)  
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
DT 01-NAR-2003 (TREMELrel. 23, Last annotation update)  
DE Spinal cord-derived growth factor.  
GN SCDGF.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=white leghorn; TISSUE=Spinal cord;  
RX MEDLINE=20317014; PubMed=10858496;  
RA Hamada T., Ui-Tei K., Miyata Y.;  
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique  
member of the PDGF/VEGF family.";  
RL FEBS Lett. 475:97-102 (2000).  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AB033829; BAB03265.1; --  
DR InterPro; IPR000859; CUB\_domain.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00341; PDGF; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS0278; PDGF 2; 1.  
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 84.0%; Score 1552; DB 13; Length 345;  
Best Local Similarity 80.3%; Pred. No. 2.3e-138;  
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAEISLSSKQLSSDKQNGVDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLTSALAGRRHGAASDLSSKFSFPGAQNGVDPQHEKIITVTSGSIHS 60  
QY 61 PKFPHYPRNMYLVWRLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEPSPGSLV 120  
DB 61 PKFPHYPRNTVLWRLVAVDENVWQLTFDERFGLDEDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIMPOVTTTSPSVLPSS 180  
DB 121 GRWCGSSVPSQISKGNQIRIRFVSDEYFPSPGFCIHYTLVPHHTAPSPSSLPSS 180  
QY 181 LSLLDNLNNAVTAFTLEELIRYLEPDRWQVLDLSYKPTWQLLGKAFYLGKSKVYNLNL 240  
DB 181 LPLDLNNAVAGFSTVEELIRYLEPDRWQVLDLSYKPTWQLLGKAFYHGRSKRVVDNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
DB 241 LKEEVRLVLSCTPRNFSVSIRELKRDTTFWPLCLLVKRCGNCACCHQNCNECCQIPYK 300  
QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKGRVGLHLSLTDVPLEHHEECDCVCKGNSEG 345

## RESULT 8

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
ID Q8K429 PRELIMINARY; PRT; 258 AA.  
AC Q8K429  
DT 01-OCT-2002 (TREMELrel. 22, Created)  
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
DT 01-NAR-2003 (TREMELrel. 23, Last annotation update)  
DE Platelet-derived growth factor C (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-Sprague-Dawley; TISSUE=Skin;  
 RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;  
 RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound  
 Healing";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AF508348; AAM47265.1; -;  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000072; PD\_growth\_factor.  
 DR Pfam; PF00431; CUB; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS50278; PDGF\_2; 1.  
 FT NON TER 1  
 FT 258 258  
 SQ SEQUENCE 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;

Query Match 74.4%; Score 1375; DB 11; Length 258;  
 Best Local Similarity 96.9%; Pred. No. 8.6e-122;  
 Matches 250; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 42 QDPHERVVTISGSIHSPKPHPTPRNMVLVAVDENVRQLTDFRFGLEDPEP 101  
 DB 1 QDPHERVVTISGSIHSPKPHPTPRNTVLVAVDENVRQLTDFRFGLEDPEP 60  
 QY 102 DICKYDFVEVEPSDGSVLGRWCGSGTVPGKTSKGNHIRIRFVSDEYPPSPGFCIHY 161  
 DB 61 DLCKYDFVEVEPSDGSVLGRWCGSGTVPGKTSKGNHIRIRFVSDEYPPSPGFCIHY 120  
 QY 162 IIMPOVTTSPVLPPSSLSLDLNNVAVTSTLEELIRLEPDRWQDLSLYKPTWQ 221  
 DB 121 IIMPOVTTSPVLPPSSLSLDLNNVAVTSTVEELIRLEPDRWQDLSLYKPTW 180  
 QY 222 LLGKAFLYGKSKVNLNLLKEEVLYSCTPRNFSVIREELKRTDTIIFWPGCLLVKRCG 281  
 DB 181 LLGKAFLYGKSKAVNLLKEEVLYSCTPRNFSVIREELKRTDTIIFWPGCLLVKRCG 240  
 QY 282 GNCACCLHNCRCQVPR 299  
 DB 241 GNCACCLHNCRCQVPR 258

RESULT 9  
 Q9EQT1 PRELIMINARY; PRT; 370 AA.  
 ID Q9EQT1  
 AC Q9EQT1  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Spinal-cord derived growth factor-B.  
 GN RSCDGF-B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21092670; PubMed=11162582;  
 RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;  
 RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to  
 SCDGF/PDGF-C/fallotain";  
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AB052170; BAB18920.1; -;  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000072; PD\_growth\_factor.  
 DR Pfam; PF00431; CUB; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR PROSITE; PS01180; PDGF; 1.  
 DR PROSITE; PS50278; PDGF\_2; 1.  
 SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73 CRC64;

Query Match 40.8%; Score 754; DB 11; Length 370;  
 Best Local Similarity 46.2%; Pred. No. 8.5e-63;  
 Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;  
 QY 37 EQNGVQD-PRHERVVTISGSIHSPKPHPTPRNMVLVAVDENVRQLTDFRFG 95  
 DB 42 ESNHLTDLYRDRDENIRVTGTHVQSPRPNLLTWRLHS-QEKTRIQAFDHFQ 100  
 QY 96 LEDPEDDICKYDFVEVEPSDGS--VLGRWCGSGTVPGKTSKGNHIRIRFVSDEYPPSE 153  
 DB 101 LEEAENDICRYDFVEVEDVSESTVVRGWCHEKTEIPRITSTNQIKITFQDDDFVAK 160  
 QY 154 PGFCIHYII--MPQ-----VTET-----TSPSVLPSSLSLDLNNVAVTST 195  
 DB 161 PGFKIYVSFVEDFQPEAASEINWESVTSSFGVSYHSPSVM-DSTLTADALDKAIAEFT 219  
 QY 196 LELIRYLEPDRWQDLSLYKPTWOLLGKAFLYGKSKVNLNLLKEEVLYSCTPRNF 255  
 DB 220 VEDLLKYFPASQDDLENLYMDTPRYGRSY-HERKSK-VLDRLNDVYKYSCTPRNH 277  
 QY 256 SVSIREELKRTDTIIFWPGCLLVKRCGNCACCLHNCRCQVPRKVTKKYHEVLQLRP-- 313  
 DB 278 SVNLREELKLTNAVFPRLCLVQRCGNCGCGTLNWKSTCSCSGKTVKKYHEVLKPEPGH 337  
 QY 314 -KTGVKGLHSLDVALEHHEHCDCVC 339  
 DB 338 FKRRGKAKNALVDIQLDHERCDCIC 364  
 RESULT 10  
 Q9GZP0 PRELIMINARY; PRT; 370 AA.  
 ID Q9GZP0  
 AC Q9GZP0  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth  
 factor long form) (Platelet-derived growth factor D).  
 GN HSCDGF-B OR IEGF OR PDGPD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;  
 RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to  
 SCDGF/PDGF-C/fallotain";  
 RL Biochem. Biophys. Res. Commun. 0:0-0(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,  
 RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,  
 RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,  
 RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Iris;  
 RA Wistow G.;  
 RT "Iris-expressed Growth Factor (IEGF).";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11331881;  
 RA Bergsten E., Uetala M., Li X., Pietras K., Ostman A., Heldin C.H.,  
 RA Alitalo K., Eriksson U.;  
 RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-  
 receptor";  
 RL Nat. Cell Biol. 3:512-516(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.

	MEDLINE=21231380; PubMed=11331882;
RX	Larochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Vernet C.,
RA	Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RR	Burgess C.E., Fernandez B., Deegler L.R., Rittman B., Shinkets J.,
RRR	Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT	"PDGF D, A Novel Protease-Activated Growth Factor.";
RFT	Nat. Cell Biol. 3:517-521(2001).
CC	-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR	EMBL; AB033832; BAB18903.1; -
DR	EMBL; AF113216; BAG39287.1; -
DR	EMBL; AY027517; AAK20081.1; -
DR	EMBL; AF336376; AAK56136.1; -
DR	EMBL; AF335584; AAK38840.1; -
DR	InterPro; IPR000859; CUB_domain.
DR	InterPro; IPR000072; PD_growth_factor.
DR	InterPro; IPR000531; TonB_boxC.
DR	Pfam; PF00431; CUB; 1.
DR	SMART; SM00141; PDGF; 1.
DR	PROSITE; PS01180; CUB; 1.
DR	PROSITE; PS0278; PDGF 2; 1.
DR	PROSITE; PS00430; TONB_DEPENDENT_REC.1; 1.
SQ	SEQUENCE 370 AA; 43848 MW; D387F485E7BB7674 CRC64;
	Query Match 40.7%; Score 752; DB 4; Length 370;
	Best Local Similarity 45.3%; Pred. No. 1.3e-62;
	Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;
QY	37 EQNGVQD-PHREVVTISGNSTHSPPHTYPRNMVLVAVDENVRILTDEBERG 95
Db	42 ESNHLTDLYXRDETQVKGNGYVQSPPFPNSPRLNLTWRLHS-QENTRIQLVPDNQFG 100
QY	96 LEDPEDIDCKYDFVEPEPSDGSL--GRWCGSVTPGKQTSGKNHIRIRVSDYPEPSE 153
Db	101 LEAENDICRYDFVEVEDISETSIIRGWCCHKKEVPPIKRSTNQIKITFKSDDYFAVK 160
QY	154 PGFCIHYSII---MPQVETTT-----SPSVLPSSLSLDLNNVAFTAEST 195
Db	161 PGFKIYVSLEDPQAAASETNWBSVTSISGVSYNSPSTDTP-TLIADALDKKIAEPDT 219
QY	196 LEELIRYLEPDRQVDLDSLYKPTWOLLGKAFLYGKSKSVNLMLLKBEVLYSCTPRNF 255
Db	220 VEDLLKFNPESQBEDLENMYYLTPRVGRSY-HDRKSK-VDLDELNDDAKRYCTPRNY 277
QY	256 SVSIREELKRTDIFWPGLLVKRCGGNCACLNHCNECQCVPKRVTKYHEVLQLRP-- 313
Db	278 SVNIREELKANVVFFPRCLLVQRCGNGCGTWNRSCTCN SGKTVKKYHEVLQFEFGH 337
QY	314 -KTGVKGLHSLTDVALEHHCEDCVC 339
Db	338 IKRRGRAKTWALVDIQLDHHERCDCIC 364
RESULT 11	
Q9BW5	PRELIMINARY; PRT; 364 AA.
ID Q9BW5	
AC Q9BW5	01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001	(TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003	(TrEMBLrel. 23, Last annotation update)
DE DE	Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).
DE DE	IEGF.
GN OS	Homo sapiens (Human).
OC OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_Taxid=9606;	[1]
RE SEQUENCE FROM N.A.	
RP RP	TISSUE=Iris;
RA RA	Wistow G.;
RT RT	"Iris-expressed Growth Factor (IEGF).";
RL RL	Submitted (Feb-2001)to the ENMBL/GenBank/DDBJ databases.





